

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 27, 2005, 13:35:45 / Search time 54 Seconds

(without alignments)
2838.047 Million cell updates/sec

Title: US-10-017-216-2

Perfect score: 10490
Sequence: 1 MKFKYGANPLDAGAEPI.....QNGEIRQVKSVALRTDVC 2053

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6C_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10022.5	95.5	2054	US-10-028-946-2	Sequence 2, App1
2	9487.5	90.4	1958	US-10-028-946-4	Sequence 4, App1
3	2430	23.2	497	US-09-804-471A-2	Sequence 2, App1
4	2430	23.2	497	US-10-338-709-2	Sequence 2, App1
5	2165.5	20.6	494	US-09-804-471A-4	Sequence 4, App1
6	2165.5	20.6	494	US-10-338-709-4	Sequence 4, App1
7	1277	12.2	257	US-09-916-204-2	Sequence 2, App1
8	1277	12.2	257	US-10-282-048-2	Sequence 2, App1
9	1253	11.9	1388	US-08-685-576-1	Sequence 1, App1
10	1250.5	11.9	1354	US-08-685-871-2	Sequence 2, App1
11	1249.5	11.9	1388	US-09-976-594-296	Sequence 2, App1
12	1247.5	11.9	1388	US-08-685-576-4	Sequence 4, App1
13	1173	11.2	251	US-09-916-204-4	Sequence 4, App1
14	1173	11.2	251	US-10-282-048-4	Sequence 4, App1
15	1170	11.2	251	US-09-916-204-5	Sequence 5, App1
16	1170	11.2	251	US-09-916-204-6	Sequence 6, App1
17	1170	11.2	251	US-10-282-048-5	Sequence 5, App1
18	1170	11.2	251	US-10-282-048-6	Sequence 6, App1
19	1043.5	9.9	900	US-08-630-822A-62	Sequence 62, App1
20	1043.5	9.9	900	US-09-005-069-62	Sequence 62, App1
21	1043.5	9.9	900	US-09-171-156A-21	Sequence 21, App1
22	1043.5	9.9	900	US-09-004-730A-21	Sequence 21, App1
23	1043.5	9.9	900	US-08-981-799A-21	Sequence 21, App1
24	896.5	8.5	509	US-09-949-016-8511	Sequence 5811, App1
25	847.5	8.1	420	US-08-685-871-58	Sequence 58, App1
26	843.5	8.0	582	US-08-422-699A-9	Sequence 9, App1
27	843.5	8.0	582	US-08-422-706B-9	Sequence 9, App1

28	830.5	7.9	420	US-08-685-871-59	Sequence 59, App1
29	799.5	7.6	638	US-08-422-706B-11	Sequence 11, App1
30	799.5	7.6	638	US-08-422-706B-11	Sequence 11, App1
31	776	7.4	555	US-08-484-044-6	Sequence 6, App1
32	706.5	6.7	479	US-09-442-100-13	Sequence 13, App1
33	706.5	6.7	479	US-08-939-106-13	Sequence 13, App1
34	706.5	6.7	479	US-08-939-106-13	Sequence 13, App1
35	691	6.6	526	US-09-442-100-13	Sequence 13, App1
36	691	6.6	526	US-08-939-106-12	Sequence 12, App1
37	691	6.6	526	US-09-442-100-12	Sequence 12, App1
38	677.5	6.5	719	US-09-588-256-2	Sequence 2, App1
39	673	6.4	404	US-08-860-150-3	Sequence 3, App1
40	673	6.4	404	US-09-338-133-3	Sequence 3, App1
41	668	6.4	464	US-08-878-988-4	Sequence 4, App1
42	668	6.4	464	US-09-272-798-4	Sequence 4, App1
43	665.5	6.3	465	US-08-878-989-18	Sequence 18, App1
44	665.5	6.3	465	US-08-860-150-7	Sequence 7, App1
45	665.5	6.3	465	US-09-338-133-7	Sequence 7, App1

ALIGNMENTS

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RESULT 1
US-10-028-946-2
; Sequence 2, Application US/10028946
; Patent No. 6734009
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanhuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fiddle, Carl Johan
; TITLE OF INVENTION: NO. 6734009 Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR APPLICATION NUMBER: 2001-12-20
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-946-2
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Query Match 95.5%; Score 10022.5; DB 4; Length 2054;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1979; Conservative 3; Mismatches 5; Indels 81; Gaps 3;

QY	1	MKFKYGANPLDAGAEPIASRASRLNLFQGGKPEFTQGMPLSRGIIIDALFVLF	60
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QY	61	ECSPALMKIKHVSFNFKYSSTIAELQELPSAKDFEVSIVGGCAEVOVVEKATG	120
DB	61	ECSPALMKIKHVSFNFKYSSTIAELQELPSAKDFEVSIVGGCAEVOVVEKATG	120
QY	121	DIYAKWKKKKLLAQEOVSPFEERNILSSTSPWIPOLQYAFODKNNLYLMEYOPGG	180
DB	121	DIYAKWKKKKLLAQEOVSPFEERNILSSTSPWIPOLQYAFODKNNLYLMEYOPGG	180
QY	181	DILSLINRYEDQDENLLOFYLAELILAVSHVLMGYVHRDIKPNILVDRGTGILYDF	240
DB	181	DILSLINRYEDQDENLLOFYLAELILAVSHVLMGYVHRDIKPNILVDRGTGILYDF	240
QY	241	GSAAGNSKNKYNNAKLPIGTDPDYNAPEYLTYWNGGKGTGIDCDWMSVGIAYEMTGR	300
DB	241	GSAAGNSKNKYNNAKLPIGTDPDYNAPEYLTYWNGGKGTGIDCDWMSVGIAYEMTGR	300
QY	301	SPFAGTSARTFNNIMNFQRLKPPDDPKVSDFLDLIQLSLCGKERTKEGGLCHPFF	360
DB	301	SPFAGTSARTFNNIMNFQRLKPPDDPKVSDFLDLIQLSLCGKERTKEGGLCHPFF	360

QY	361	SKIDMNNIRNSPPFPVPLTKSDDDTNSPNDPEKNSWSSSPCOLSPSGFGSEELPVPFGS	420
Db	361	SKIDMNNIRNSPPFPVPLTKSDDDTNSPNDPEKNSWSSSPCOLSPSGFGSEELPVPFGS	420
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Db	421	YSKALGILIGREESVVSGLDSPAITSMEKKLLINSKELODPODKCHMEOMENTLHRVS	480
QY	481	EVEAVLSQKEVELKASEFQESLLEODLATYTTTESSSLKRSIPQARMEVSOEDDKAOLH	540
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QY	541	DIREOSRLQEIKEOEYOAOYEENKLMNNQOEPLVSARRSDIYSEELRESRLAAEFK	600
Db	541	DIREOSRLQEIKEOEYOAOYEENKLMNNQOEPLVSARRSDIYSEELRESRLAAEFK	600
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Db	649	----AKESAEBELKLONRDESSSEIRKQVYEAERBSHLENKYRLETMERRENRRLKID	704
QY	705	IOTKSQOIQOMADKILBELBEKHREAOVSAOHLVHLKQEQHYEKIKVLDMQIKDOLAD	764
Db	721	IOTKSQOIQOMADKILBELBEKHREAOVSAOHLVHLKQEQHYEKIKVLDMQIKDOLAD	780
QY	765	KETLENMNOHRHEENHEKGLISBECKAMINMDSKTSIBJORIYELBANGLANSSLFT	824
Db	761	KETLENMNOHRHEENHEKGLISBECKAMINMDSKTSIBJORIYELBANGLANSSLFT	840
QY	825	QRMNKAQOEMISSELSQOKFVYLETQAGKLEAQRKLEBQLEKISHODSDKNRLLELSTR	884
Db	841	QRMNKAQOEMISSELSQOKFVYLETQAGKLEAQRKLEBQLEKISHODSDKNRLLELSTR	900
QY	885	REVSLEHBEQKLELKRQULTEILOLSIQEBSQITLQARALBESOLROAKTELEETTAEA	944
Db	901	REVSLEHBEQKLELKRQULTEILOLSIQEBSQITLQARALBESOLROAKTELEETTAEA	960
QY	945	BEIIOALTAHREIQRKFPDALNSCTVITDLEBOLQJTEONAELNNOFYLISQOLDEAS	1004
Db	961	BEIIOALTAHREIQRKFPDALNSCTVITDLEBOLQJTEONAELNNOFYLISQOLDEAS	1020
QY	1005	GANDEIVOLRSSEVDHRLREITEREMQOLTSQKOTMEALKTTCMLBEQVMDLEAINDEILE	1064
Db	1021	GANDEIVOLRSSEVDHRLREITEREMQOLTSQKOTMEALKTTCMLBEQVMDLEAINDEILE	1080
QY	1065	KERQWEARMSVUGDKSQPECVRELOMRLTEKQSRARAOORTTESQOVVELVKEKHA	1124
Db	1081	KERQWEARMSVUGDKSQPECVRELOMRLTEKQSRARAOORTTESQOVVELVKEKHA	1140
QY	1125	ETILALQOALKEQALKAESLSIDKLNLDLEKKHMLENNARSLQOKLETERELKORLLEBOAK	1184
Db	1141	ETILALQOALKEQALKAESLSIDKLNLDLEKKHMLENNARSLQOKLETERELKORLLEBOAK	1200
QY	1185	LOOQOMDLOQNNHIFRUTQCIQELADPADILKTERSPSLBYOLNIQVLYSHEKYKMEGTSISQ	1244
Db	1201	LOOQOMDLOQNNHIFRUTQCIQELADPADILKTERSPSLBYOLNIQVLYSHEKYKMEGTSISQ	1260
QY	1245	OTKRLDIFLOAKMDOPAKKKKGKGFSSRKEDPALPTQVPOVMEYLKALKEKAKACALEEA	1304
Db	1261	OTKRLDIFLOAKMDOPAKKKKGKGFSSRKEDPALPTQVPOVMEYLKALKEKAKACALEEA	1305
QY	1305	LOKTRIELRSABEAAHRAVTDHPHPSTPATARQOIIAMSAIVRSPEHOPSAMSLIAPSS	1364
Db	1306	LOKTRIELRSABEAAHRAVTDHPHPSTPATARQOIIAMSAIVRSPEHOPSAMSLIAPSS	1365
QY	1365	RKRESSTPEFSRRLKERNNHNIPIRPNVGLMRAKTKCAVCLDTPYHFRQASKCLBEOVM	1424
Db	1366	RKRESSTPEFSRRLKERNNHNIPIRPNVGLMRAKTKCAVCLDTPYHFRQASKCLBEOVM	1425
QY	1425	CHPKCSTCLPATCGHPAEVATHTETAFCBDKNNSSDLOTKEBSSSLHEGMWKVPRNNKR	1484

[illegible]

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QY 121 DIYAMKVMKKALLAEOVSFFEEERNISRSTSPWIPQLOVAFODKXHYLYMEEXOPGG 180
DB 121 DIYAMKVMKKALLAEOVSFFEEERNISRSTSPWIPQLOVAFODKXHYLYMEEXOPGG 180
QY 121 DIYAMKVMKKALLAEOVSFFEEERNISRSTSPWIPQLOVAFODKXHYLYMEEXOPGG 180
DB 121 DIYAMKVMKKALLAEOVSFFEEERNISRSTSPWIPQLOVAFODKXHYLYMEEXOPGG 180
QY 181 DLSLLNRYEDQDENILIOFYLAELILAVHSVHLMGVHDIKPENILYDRTHIKLVDF 240
DB 181 DLSLLNRYEDQDENILIOFYLAELILAVHSVHLMGVHDIKPENILYDRTHIKLVDF 240
QY 241 GSAKAKNSNMVNAKPIGTPDYMAPEVLTVMNGDGKGTGLDCCDMWSVVIAYEMIYGR 300
DB 241 GSAKAKNSNMVNAKPIGTPDYMAPEVLTVMNGDGKGTGLDCCDMWSVVIAYEMIYGR 300
QY 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSDFLDIOGLCGOKERLKFEGLCCHPFF 360
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DB 705 IQTKSOQIQOMADKILELEEKHREAQVSAQHEVHLKQKQHEBKIKVLNDQIKKDLAD 764
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DB 765 KETLENNQORHEEAHEKGLISEQOKAMITAMDSKISLEFORIVEISEANKLAANSGLFT 824
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DB 825 QORAKKAOEEMISLROOKFYLETOAGKLEAONKRLKEBQLEKISHOHSQDNRLLEETRL 884
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DB 841 QORAKKAOEEMISLROOKFYLETOAGKLEAONKRLKEBQLEKISHOHSQDNRLLEETRL 900
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DB 885 REVLSLEHEBQKLEKLOTELQSLQERESQALQAPARALSESOLRQAKTELEETTTABA 944
QY 901 REVLSLEHEBQKLEKLOTELQSLQERESQALQAPARALSESOLRQAKTELEETTTABA 960
DB 901 REVLSLEHEBQKLEKLOTELQSLQERESQALQAPARALSESOLRQAKTELEETTTABA 960
QY 945 EEBEIOALTARDEIORKFDALRNSCTVITDLEBQALQUTEDNANLANNONYLSKOIDEAS 1004
DB 945 EEBEIOALTARDEIORKFDALRNSCTVITDLEBQALQUTEDNANLANNONYLSKOIDEAS 1004
QY 961 EEBEIOALTARDEIORKFDALRNSCTVITDLEBQALQUTEDNANLANNONYLSKOIDEAS 1020
DB 961 EEBEIOALTARDEIORKFDALRNSCTVITDLEBQALQUTEDNANLANNONYLSKOIDEAS 1020
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DB 1141 BITALQOALKEOKLKAESLSDKLNDLEKKHAMELNNASLSQOKLETTERELKORLLEBOAK 1200
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DB 1185 LQOQMDLOQKNIIFRLTOGLQEALDRADLLKTERSDLEYOLENIQVLYSHEKVMESTISQ 1244
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DB 1201 LQOQMDLOQKNIIFRLTOGLQEALDRADLLKTERSDLEYOLENIQVLYSHEKVMESTISQ 1260
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DB 1261 QTKLIDFLOAKNDQPAKKKKGLFSRKKEPALPTQVPLQYBELKALAEKAKCALEBA 1305
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DB 1305 LOKTRIELSAREBAHRKATDHPHSTPATARQOAMSAIYRSPHOSAMSILAPSS 1364
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DB 1366 RKRSESTPEEFBRRLKERHNNIPIHFVGLMMBATKCAVCLDTYHFGHQAQKCEQVM 1425
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QY 1485 GQOQMDRKYIVLEGSVLLYDNEAREAGORPYEPEELCLPDGVSITHGAVGASELANTAK 1544
DB 1485 GQOQMDRKYIVLEGSVLLYDNEAREAGORPYEPEELCLPDGVSITHGAVGASELANTAK 1544
QY 1545 A-----EKAEADAKL 1554
DB 1545 A-----EKAEADAKL 1554
QY 1546 ADVPYILKMHSPHTTCWPGRTLYLLAPSPDKQKRVNTALSESVMAGVRSREAEADAKL 1605
DB 1546 ADVPYILKMHSPHTTCWPGRTLYLLAPSPDKQKRVNTALSESVMAGVRSREAEADAKL 1605
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DB 1555 LGNSLILKEGDRDLDMNCTLPSPDOVYLVTEBGLYALNVLKNSLTHVPGIGAVFOIYII 1614
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DB 1666 KOLEKXLMTAGERBALCVDVVKVYKOSLAQSHLPAPODISPINIFAVKCGHLFGAGKIN 1725
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DB 1675 GLCICAMPKSVIILRYNNELSKYCIKKEIETSEPCSIHFTNYSLITGNKPYEIDMKO 1734
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QY 1846 RTDDLKMSRLPLAFAREBYLVTHHNSLEVIEIQARSSAGTPARAYLIDIPNRYLGPAI 1905
DB 1846 RTDDLKMSRLPLAFAREBYLVTHHNSLEVIEIQARSSAGTPARAYLIDIPNRYLGPAI 1905
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RESULT 3
US-09-804-471A-2
; Sequence 2, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 497

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TYPE: PRT
ORGANISM: Human
US-09-804-471A-2

Query Match 23.2%; Score 2430; DB 4; Length 497;
Best Local Similarity 99.1%; Pred. No. 1.3e-117;
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MLKFKYGARNPLDGAAPRIASASRLNLFQGGKPPFMTQOQMSPLSRGGILDALFVLF 60
DB 1 MLKFKYGARNPLDGAAPRIASASRLNLFQGGKPPFMTQOQMSPLSRGGILDALFVLF 60
QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEYQVREKATG 120
DB 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEYQVREKATG 120
QY 121 DIYAMKVMKKALLAQEQVSFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYQPG 180
DB 121 DIYAMKVMKKALLAQEQVSFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYQPG 180
QY 181 DLISLNRVEDQDENLQFYLAELILAVSHVMGYHRDIPKPNILVDRGHIKLVDF 240
DB 181 DLISLNRVEDQDENLQFYLAELILAVSHVMGYHRDIPKPNILVDRGHIKLVDF 240
QY 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMTYGR 300
DB 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMTYGR 300
QY 301 SPFAEGTSARTNNINMFORFLKFPDDPKVSSDFLDLQSLCGQERLKFBGLCCHPF 360
DB 301 SPFAEGTSARTNNINMFORFLKFPDDPKVSSDFLDLQSLCGQERLKFBGLCCHPF 360
QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPKNSWSSPCQLSPGSGEELPFVGS 420
DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPKNSWSSPCQLSPGSGEELPFVGS 420
QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLIKSKELQDSQDKCHKV 468
DB 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLIKSKELQDSQDKCHKV 468
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RESULT 4
US-10-238-709-2
Sequence 2, Application us/10238709
Patent No. 6680188

GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL001164DIV
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 497
TYPE: PRT
ORGANISM: Human
US-10-238-709-2

Query Match 23.2%; Score 2430; DB 4; Length 497;
Best Local Similarity 99.1%; Pred. No. 1.3e-117;
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MLKFKYGARNPLDGAAPRIASASRLNLFQGGKPPFMTQOQMSPLSRGGILDALFVLF 60
DB 1 MLKFKYGARNPLDGAAPRIASASRLNLFQGGKPPFMTQOQMSPLSRGGILDALFVLF 60
QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEYQVREKATG 120
DB 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEYQVREKATG 120
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QY 121 DIYAMKVMKKALLAQEQVSFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYQPG 180
DB 121 DIYAMKVMKKALLAQEQVSFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYQPG 180
QY 181 DLISLNRVEDQDENLQFYLAELILAVSHVMGYHRDIPKPNILVDRGHIKLVDF 240
DB 181 DLISLNRVEDQDENLQFYLAELILAVSHVMGYHRDIPKPNILVDRGHIKLVDF 240
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QY 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMTYGR 300
DB 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMTYGR 300
QY 301 SPFAEGTSARTNNINMFORFLKFPDDPKVSSDFLDLQSLCGQERLKFBGLCCHPF 360
DB 301 SPFAEGTSARTNNINMFORFLKFPDDPKVSSDFLDLQSLCGQERLKFBGLCCHPF 360
QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPKNSWSSPCQLSPGSGEELPFVGS 420
DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPKNSWSSPCQLSPGSGEELPFVGS 420
QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLIKSKELQDSQDKCHKV 468
DB 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLIKSKELQDSQDKCHKV 468
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RESULT 5
US-09-804-471A-4
Sequence 4, Application us/09804471A
Patent No. 6479269

GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL001164
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 494
TYPE: PRT
ORGANISM: Mus Musculus
US-09-804-471A-4

Query Match 20.6%; Score 2165.5; DB 4; Length 494;
Best Local Similarity 87.8%; Pred. No. 5.2e-104;
Matches 411; Conservative 26; Mismatches 30; Indels 1; Gaps 1;

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QY 1 MLKFKYGARNPLDGAAPRIASASRLNLFQGGKPPFMTQOQMSPLSRGGILDALFVLF 60
DB 1 MLKFKYGARNPEASASEPIASASRLNLFQGGKPPMTQOQMSALSREGLDALFVLF 60
QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEYQVREKATG 120
DB 61 ECSQPALMKHGVSNFVQKYSDTIAELRELQPSARDFEVRSLVGCCHFAEYQVREKATG 120
QY 121 DIYAMKVMKKALLAQEQVSFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYQPG 180
DB 121 DIYAMKVMKKALLAQEQVSFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYQPG 180
QY 181 DLISLNRVEDQDENLQFYLAELILAVSHVMGYHRDIPKPNILVDRGHIKLVDF 240
DB 181 DLISLNRVEDQDENLQFYLAELILAVSHVMGYHRDIPKPNILVDRGHIKLVDF 240
QY 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMTYGR 300
DB 241 GSAAKNSNK-VDAKLPIGTPDYMAPEVLTVMNEDRGITGLDCDMSVGVIAEMTYGR 299
QY 301 SPFAEGTSARTNNINMFORFLKFPDDPKVSSDFLDLQSLCGQERLKFBGLCCHPF 360
DB 301 TPFEGETSARTNNINMFORFLKFPDDPKVSSDFLDLQSLCGQERLKFBGLCCHPF 359
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QY 361 SKIDMNNINSPPPFVPTLKSDDDTSNFBPEKNSVSSPCOLSPSGFGEELPFVGF 420
DB 360 AKIDMNNINSPPPFVPTLKSDDDTSNFBPEKNSVAFLLCPABFLASGEBELPFVGF 419
QY 421 YSKALGILGRSSSVSGLDSPAKTSSMEKKLLIKSKELODSDQKCHKM 468
DB 420 YSKALGILGRSSSVSGLDSPAKVSSMEKKLLIKSKELODSDQKCHKV 467

RESULT 6
US-10-238-709-4
; Sequence 4, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-238-709-4

Query Match 20.6%; Score 216.5; DB 4; Length 494;
Best Local Similarity 87.8%; Pred. No. 5.2e-104;
Matches 411; Conservative 26; Mismatches 30; Indels 1; Gaps 1;

QY 1 MUKFYGARNPIDAGAAEPIASRASRLNLFQGGKPPFTQOQMSPLSREGIIDLALFVLF 60
DB 1 MUKFYGARNPIDAGAAEPIASRASRLNLFQGGKPPFTQOQMSPLSREGIIDLALFVLF 60
QY 61 EESOPALMKIKIVSNFVKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEYQVAREKATG 120
DB 61 EESOPALMKIKIVSNFVKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEYQVAREKATG 120
QY 121 DIYANKVMKKKALLAQEOVSFPEEERNILSRSTSPWIPOLQYAFODKXHLVMEYQPGG 180
DB 121 DIYANKVMKKKALLAQEOVSFPEEERNILSRSTSPWIPOLQYAFODKXHLVMEYQPGG 180
QY 181 DLSTLNRYEDQDENLQIIFYLAELILAVSHVLMGYVARDIKPENILVDRGHIKLVDF 240
DB 181 DLSTLNRYEDQDENLQIIFYLAELILAVSHVLMGYVARDIKPENILVDRGHIKLVDF 240
QY 241 GSAAKNSKNVNAKLPITGTPYMAPEVLTVMNEDRGTGGLDCMWSGVVAYEYVYK 299
DB 241 GSAAKNSKNVNAKLPITGTPYMAPEVLTVMNEDRGTGGLDCMWSGVVAYEYVYK 299
QY 301 SPFAGTSARTFNINNFQRLKFPDDPVSSDPLDLSLQCGEKRLKPFGLCHPFF 360
DB 300 TPFTEGTSARTFNINNFQRLKFPDDPVSSDPLDLSLQCGEKRLKPFGLCHPFF 359
QY 361 SKIDMNNINSPPPFVPTLKSDDDTSNFBPEKNSVSSPCOLSPSGFGEELPFVGF 420
DB 360 AKIDMNNINSPPPFVPTLKSDDDTSNFBPEKNSVAFLLCPABFLASGEBELPFVGF 419
QY 421 YSKALGILGRSSSVSGLDSPAKTSSMEKKLLIKSKELODSDQKCHKM 468
DB 420 YSKALGILGRSSSVSGLDSPAKVSSMEKKLLIKSKELODSDQKCHKV 467

RESULT 7
US-09-916-204-2
; Sequence 2, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
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; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
US-09-916-204-2

Query Match 12.2%; Score 1277; DB 4; Length 257;
Best Local Similarity 99.2%; Pred. No. 1.3e-58;
Matches 250; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MUKFYGARNPIDAGAAEPIASRASRLNLFQGGKPPFTQOQMSPLSREGIIDLALFVLF 60
DB 1 MUKFYGARNPIDAGAAEPIASRASRLNLFQGGKPPFTQOQMSPLSREGIIDLALFVLF 60
QY 61 EESOPALMKIKIVSNFVKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEYQVAREKATG 120
DB 61 EESOPALMKIKIVSNFVKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEYQVAREKATG 120
QY 121 DIYANKVMKKKALLAQEOVSFPEEERNILSRSTSPWIPOLQYAFODKXHLVMEYQPGG 180
DB 121 DIYANKVMKKKALLAQEOVSFPEEERNILSRSTSPWIPOLQYAFODKXHLVMEYQPGG 180
QY 181 DLSTLNRYEDQDENLQIIFYLAELILAVSHVLMGYVARDIKPENILVDRGHIKLVDF 240
DB 181 DLSTLNRYEDQDENLQIIFYLAELILAVSHVLMGYVARDIKPENILVDRGHIKLVDF 240
QY 241 GSAAKNSKNV 252
DB 241 GSAAKNSKNV 252

RESULT 8
US-10-282-048-2
; Sequence 2, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
US-10-282-048-2

Query Match 12.2%; Score 1277; DB 4; Length 257;
Best Local Similarity 99.2%; Pred. No. 1.3e-58;
Matches 250; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MUKFYGARNPIDAGAAEPIASRASRLNLFQGGKPPFTQOQMSPLSREGIIDLALFVLF 60
DB 1 MUKFYGARNPIDAGAAEPIASRASRLNLFQGGKPPFTQOQMSPLSREGIIDLALFVLF 60
QY 61 EESOPALMKIKIVSNFVKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEYQVAREKATG 120
DB 61 EESOPALMKIKIVSNFVKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEYQVAREKATG 120
QY 121 DIYANKVMKKKALLAQEOVSFPEEERNILSRSTSPWIPOLQYAFODKXHLVMEYQPGG 180
DB 121 DIYANKVMKKKALLAQEOVSFPEEERNILSRSTSPWIPOLQYAFODKXHLVMEYQPGG 180
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Qy	161	DLSLNRYEQOLJENLQFYLAELILAVSHVLMGYVRIRIKENILVDTGHIKLVDF	240
Db	181	DLSLNRYEQOLJENLQFYLAELILAVSHVLMGYVRIRIKENILVDTGHIKLVDF	240
Qy	241	GSAAKMSNNKRV	252
Db	241	GSAAKMSNNKRV	252
RESULT 9			
	US-08-685-576-1		
	Sequence 1, Application US/08685576		
	Patent No. 5906819		
	GENERAL INFORMATION:		
	APPLICANT: Kaibuchi, Koza		
	APPLICANT: Iwamatsu, Akihito		
	APPLICANT: Nakano, Takeshi		
	APPLICANT: Ito, Masaaki		
	APPLICANT: Takahashi, No. 5906819uaki		
	TITLE OF INVENTION: RHO TARGET PROTEIN RHO-KINASE		
	NUMBER OF SEQUENCES: 16		
	CORRESPONDENCE ADDRESS:		
	ADDRESSEE: Foley & Lardner		
	STREET: 3000 K Street, N.W., Suite 500		
	CITY: Washington		
	STATE: D.C.		
	COUNTRY: USA		
	ZIP: 20007-5109		
	COMPUTER READABLE FORM:		
	MEDIUM TYPE: Floppy disk		
	COMPUTER: IBM PC compatible		
	OPERATING SYSTEM: PC-DOS/MS-DOS		
	SOFTWARE: PatentIn Release #1.0, Version #1.30		
	CURRENT APPLICATION DATA:		
	APPLICATION NUMBER: US/08/685,576		
	FILING DATE: 24-JUL-1996		
	CLASSIFICATION: 435		
	PRIOR APPLICATION DATA:		
	APPLICATION NUMBER: JP 7-325129		
	FILING DATE: 20-NOV-1995		
	PRIOR APPLICATION DATA:		
	APPLICATION NUMBER: JP 8-17150		
	FILING DATE: 05-JAN-1996		
	PRIOR APPLICATION DATA:		
	APPLICATION NUMBER: JP 8-131206		
	FILING DATE: 26-APR-1996		
	ATTORNEY/AGENT INFORMATION:		
	NAME: Benl, Stephen A.		
	REGISTRATION NUMBER: 29,768		
	REFERENCE/DOCKET NUMBER: 16887/843		
	TELECOMMUNICATION INFORMATION:		
	TELEPHONE: (202)672-5300		
	TELEFAX: (202)672-5399		
	TELEX: 904136		
	INFORMATION FOR SEQ ID NO: 1:		
	SEQUENCE CHARACTERISTICS:		
	LENGTH: 1388 amino acids		
	TYPE: amino acid		
	TOPOLOGY: linear		
	MOLECULE TYPE: protein		
	US-08-685-576-1		
Qy	Query Match	11.9%;	Score 1253; DB 2; Length 1388;
Db	Best Local Similarity	26.1%;	Pred. No. 1,4e-56;
	Matches 394; Conservative 251;	Mismatches 507;	Indels 320; Gaps 50
Qy	15 GAEPYA---SBRASRLNLFEGGKPPMTQOQMSPLSRREGILDALFVLPFGCSQPALMKIK	71	
Db	12 GAFVNSGGGAGASR-----QRLTALRLNDPRSPINVESILDLGNLPLVLDLDFPALRRKK	66	
Qy	72 HSNFVRKYSDTLAELOELQPSAKDPEVNSLVGCGHFAVQVVRKATSDIYAMKVMKK	131	

Db	67	NIDNFAIRYEKUYKKGIRGLQMAKEDVDVUVKISRGAFGEVQVLRHAKASQVAVMKLISKE	126
Qy	132	ALLAQEOVSFPEEBERNILSSTSPWIPOLQYAFQDNKHLTYMEYQPGDLSILARIED	191
Db	127	EMIKRSDSAFWEERDIMAFAISPWVQVLCFAEQDDCYLTYMWEVWPGGLVAINMKNYD-	185
Qy	192	QDENLQPIYLAELILAVHSHVMGYVRIPKENTILVDTGHIKLVDFCSAJKNMKNK	251
Db	186	-VPERMAKFYAEAVLALDAIHSGLHBRVAKEDPNKLLDHGHLKADFECSKMBETGM	244
Qy	252	VNAKLPCTGPDYMAPEVLTVMNGDGKGTGYLGDGWSVGIYAYEMIYGRSPFAEGTSART	311
Db	245	VHCPTAGTPTPIYSIPBYLKSQGG--GYRECDMWSVGVFLEMYLVDGTPFYADSLVGT	302
Qy	312	FNNTMNFQRLKFPDDPKVSSDFLDLIQSLICQGERKLFEG--LCSPFFSKIDWN--	366
Db	303	YSKIMDHKNSLCPEDAEISGHANMLICAFLTREVALGRNGVEIKQHPFFNDOMNMD	362
Qy	367	NIRNSPPFPVYTLKSDDTGNSPDEPKSNV--VSSPCQLSPSGSGEPLFFVFSYSKUL	425
Db	363	NIREPAAVPELSSDIDSNFDDIEDQKDVPEPFI--PKAFVGNQPLFFIGFTTYREN	419
Qy	426	GILGSESVSGLSPPA--KTSMSWEKLLIKSKELQSDQCKHMEQENTLHRVSEVE	483
Db	420	ILLS-----DSPCKENDSIQSR--KNESQEIQKKLYTBHLS-----	457
Qy	484	AVLSQKEVELKASTORSLLBODIATYITBCCSLKNSLEQARNEVSOEDKALQALHDIR	543
Db	458	-----TEIQAKEE--LEQ-----KCKSVNTELEKVAKELEBEITLRKNVESTLR	499
Qy	544	--EQSKIQELKEBOYQOUEMRYMAMNOLEEDVSVARRSDSYESELRESRLAAEFKR	601
Db	500	OLERKALLQHKNAEYQKADHEADKGRNLENDVNSLKQULEDKKNQNSQISTE----	555
Qy	602	KATCGHKLILAKQCKREVEEYAKLEKINAEQOLKIQ-----ELQEK--LEKAKER	652
Db	556	KYNQJQRUDBTNALLRTESPTARLAKTQAESKQIQOLESNNRDLQDNKCLLETAKIK	615
Qy	653	AERLEKLOÑNEDSSEGIKKVLVAEERRRSLSENKVRLETMBERRRKLADDIOTSQOI	712
Db	616	LEKEPIÑQSVLSE--RRDRTGSETINDLOGRISGLEBDVNGKILAKLELEKQOL	672
Qy	713	QOMADKIIELEKREAVSAQH-----LEVHLKQKE--QHVEEKIKVND--NOIKDL--AD	764
Db	673	Q---ERFDTLEKKNMEIDMTYQVKYIQOSLEQBEETHKATKRLADKKNKIYESIEAK	729
Qy	765	KETLENMYQRIHEEBAHEKGI--LSEOKMIMNMSKIRSLREORIVELSE---ANKLA	817
Db	730	SEAMKEMEKUSSEBRTLKQVENLLEBKRCSTLDDODKQSQCKINELLKQKOVANEDV	789
Qy	818	ANNSI-----FTORNKQAQEMISBLRQOKFYLETQAGKLEKQNRLEBQLEKIS	867
Db	790	RVLTKIEQETQKCLTQNDLKMQTOQVNTLKMS-----EKQLOQ--	829
Qy	866	HODHDKRRLLELBTRLAEVSLHHEBQKLEKQOTELQSLQJESQLOFTALQARAALÉ	927
Db	830	-----ENNHLBEMKSL-----EKQABEIKRQRQDQGMKYLQOLEMEQYFSTLYK	877
Qy	928	SOLQOAKTELEBETT--AEAEERIQALTAHDEIQRFDALRNSCTVITDLERQOLQTE	984
Db	878	TOVRELKECECKTKLCKELOQKQKQELQDERDLSLAQLE-----ITLTKADSEQLAR	929
Qy	985	DNAELINNONFYLSKQLEDAAGANDEIYQJARSEVDHLRREITEREMQLTISQKQJMEALKTT	1044
Db	930	SIABEQSYDLEKEKIMKE-----LEIKEMARHKOLETEKQATYASLEETIRTLTSD	981
Qy	1045	CTMLEEQVMDLEALNDELLEKQWEMARSTYSGE-----KSQFQRVRELORMDE	1097
Db	982	VANILAN-----EKXEILNNKLEKQEO--LSRLKQBEISAAAIKQAF-----KOLLTE	1027
Qy	1098	KQSRBARQORITRESQOVAVLAVKEHKAETIILLOOLKEQKLAESLSDKLNLEKGIAML	1157
Db	1028	RTLKQYAVNKL-----AEIMRKPEYK-----RGNDTVVRK--	1059

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Oy 1158 PMNARSLQOKJETERBELKORLLEBQAKJQOQMDLOJXNI PRITQ---GLOBALRADLYK 1214
Db 1060 EKENRKLHMEI.KSERE---KLTOQWIKYQKELNEMOAOIAESQRILOMTLTKSD--- 1113
Oy 1215 TERSDLEXYOLENIOVLY-----SHEKYMEGTIS---OQTKLIDF 1251
Db 1114 ---SDIEBLRSQLOALHIGLDSSSTIGSGPGPTLEADGFPESRLEBOWLSPLPRNNTKKRGW 1170
Oy 1252 LOAKMDOPAKKKKGJFSRRKEDPALPTQV-----PLOYNELKLALKEKARCAEL 1301
Db 1171 VKKVVYVSSKKILFYDSEQDKQSNPWWLIDIKLFHVRPVTQTDVVRADAKELPRIGQI 1230
Oy 1302 EEALOKTRIEI.LSABEAARAKAIDPHRPSRPTATRAQOIAMSAIVSPEHOPSAWSGLAP 1361
Db 1231 -----LYAN 1234
Oy 1362 PSRRKESSTP---EFSRRLKERMHNINI.PHRFVNGJLMBATKCAVCLDTVHFGROASK 1417
Db 1235 EGESKKEDEFPVEPVGKSNYI.CHKGHGFIPPLYHF-----PTWCEACMKPLMHMFKPP 1289
Oy 1418 CLECOVMCHPKC 1429
Db 1290 ALBGR-RCHIKC 1300

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1      RESULT 10
2      US-08-685-871-2
3      Sequence 2, Application US/08685871
4      Patent No. 6013499
5      GENERAL INFORMATION:
6      APPLICANT: NARUMIYA, Shuh
7      APPLICANT: IWAMATSU, Akhiro
8      TITLE OF INVENTION: RHO TARGET PROTEIN KINASE P16
9      NUMBER OF SEQUENCES: 68
10     CORRESPONDENCE ADDRESS:
11     ADDRESSEE: Foley & Lardner
12     STREET: 3000 K Street, N.W., Suite 500
13     CITY: Washington
14     STATE: D.C.
15     COUNTRY: USA
16     ZIP: 20007-5109
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: Floppy disk
19     COMPUTER: IBM PC compatible
20     OPERATING SYSTEM: PC-DOS/MS-DOS
21     SOFTWARE: PatentIn Release #1.0, Version #1.30
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/08/685,871
24     FILING DATE: 24-JUL-1996
25     CLASSIFICATION: 435
26     PRIOR APPLICATION DATA:
27     APPLICATION NUMBER: JP 8-184102
28     FILING DATE: 25-JUN-1996
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER: JP 7-262553
31     FILING DATE: 14-SEP-1995
32     ATTORNEY/AGENT INFORMATION:
33     NAME: BENT, Stephen A.
34     REGISTRATION NUMBER: 29,768
35     REFERENCE/DOCKET NUMBER: 16887/845
36     TELECOMMUNICATION INFORMATION:
37     TELEPHONE: (202)672-5300
38     TELEFAX: (202)672-5399
39     TELEX: 904136
40     INFORMATION FOR SEQ ID NO: 2:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 1354 amino acids
43     TYPE: amino acid
44     TOPOLOGY: linear
45     MOLECULE TYPE: protein
46     US-08-685-871-2

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[illegible]

Db 928 ---ROEITDKD-----HTVSRLEANSMLTKOIEILRRENEBELTEKKAEESEYLEK 977

Qy 1078 DE-----KSQECRAVEIQRMLDTEKOSBARADQITSRQVVELAVENHEALIALQQA 1132

Db 978 ESEISLTKAAFE-----KNINTERTLTKQAVNKLAIEMRKDKIRKKAANTODLKK 1030

Qy 1133 LKEOK---LKASLSLDPKLNDEKKAAMLEMNARSLOOKLETREBELKORLLEEQA---KLQ 1186

Db 1031 EKENRKLQLELNOEKEKQVAVKH-----QKEL---NDMQADLVECAHREMLQ 1077

Qy 1187 OQMDLOKNIHFRITQGLQALDRADLKTERSDLEVOLENIOVLYSHEKVMEGTISQOT 1246

Db 1078 MQLASKESDIEQRAVLKLDLSDTSVASPSAD-----ETDGNLPSR 1120

Qy 1247 KLIDFLQAKMDQPAKKKGLFSRKEDPALPTQVPLQVNEKLALKEKARCAELEALQ 1306

Db 1121 -----IEGMLSVNRRNIRYKWKQYVAVSSKILFTNDEQDKQSNPSWLDIDLKL-- 1173

Qy 1307 KTRIELRSAREEAHRAKATDHPHSTPATARQOIAMSAIVRSREHOPASMLAPSSRR 1366

Db 1174 ---FHRPVTQGDVYAAET-----EELPKIFQILVANECEC 1206

Qy 1367 KESSTPEESFRILKEKHNHNIPIRENVGLMRAKCAVCLDVIHREGKQSKLEQVWGH 1426

Db 1207 RKQVEBPVQQAQEKTFQNHKGHEFTPLYHPPANDACAKPLMHVFKPRPALBCK-RCH 1265

Qy 1427 PKGS-----TCLPATCGLPAEYATHTFAFCRDKKNSPGLQTEKPESSSLHEGM 1476

Db 1266 VKCHRDHLDKEDLIC-----PKVSYDVYTA--RDMILLACSGDEQKQWTHLV--K 1314

Qy 1477 KVPNNNRKG 1485

Db 1315 KIPKNPPSG 1323

RESULT 11

US-09-976-594-296

; Sequence 296, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 296

; LENGTH: 1388

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. 6673549 064987CD1

US-09-976-594-296

Query Match 11.9%; Score 1249.5; DB 4; Length 1388;

Beet Local Similarity 26.3%; Pred.No.2.1e-56;

Matches 391; Conservative 291; Mismatches 513; Indels 293; Gaps 47;

Qy 24 ASRLNLFQGGKPPMTQOQMSPLSRGILDALFVLFECSQPALMKITGVNPFKXYSDT 83

Db 24 ASR-----QRKLEALIRPSPSPINVESLIDGLNLSVLDELFPALKKNKNIIDFNARVEKI 78

Qy 84 IAELELOPSAKDEFVRSIVGCGHFAVQVVEKATGDIYAMKVKKKKLLAOEQVSFFE 143

Db 79 VKKIGELQKKADYDVVKVIGKAGFGEVULVHKKSKQKYAMKLSKEMIKRSDSAFW 138

Qy 144 EERNILSRSTSPWIDQLQYAFQDKNHLYLMEBYQDGDLLSLNRYEDQDLNLIQFLA 203

Db 139 EERDILAFANSPWVQVLFYAFODDRKLYMMEYMEYGGDLVNLMSYVD--VPEKMAKPYTA 196

Qy 204 ELTIAVSHVLMGYYVRDIKPENILVDRTGHIKLYDFGSAAGNSNKNVNAKLPIGTGDY 263

Db 197 EYVLALDAHSWGLIHRVYKPDNMLDKHGHKLADFGCMKDDGTGVHCTYAGTADPY 256

Qy 264 MAPEVLTWANGDGKGTGYGDCDMSVSVGLAYEMIGRSPPAGTSARTEFNINMFORFLK 323

Db 257 ISPEVLKSGQGD--GFYGRCECDMSVGVFLYEMLVGDTFPYADSLVGTYSKIMDHNSLC 314

Qy 324 FPDDPKVSDFDLTIQSLICQGERLKFEFG---LCCHPFP--SKIDWNINRSPPPFVY 378

Db 315 FPEDAEISKAKNLICAFILDRVRLGRNGVEIRQHPPFKIDQWMDNIRETAAPVVE 374

Qy 379 LKSDDTNSFDEPKNW--VSSPCQLSPSGFGEELPVGVSYSALGILGRSESVVG 437

Db 375 LSSDIDSNFDDIEDKGDVETFP--PAFVGNQLPFIQFYTYENLILS----- 423

Qy 438 LQSPA--KTSMEKULLIKSEKLODSQDKCHKMEOENTRLHRRVSEVAVLQKEVELKA 495

Db 424 -DSPSCRENDSTQSR--KNBESQETQKLYTEHLN-----EMQA 462

Qy 496 SETQSRILBODLATYITECSLSLEQARMEVSQF-----DKALQLLHDIREQRL 549

Db 463 KEE---LEQ-----KCKSVNTRLEKTAKELEBEITLLKSVESALROL--EKEKL 507

Qy 550 QETQEQYQAOVEMRLMNNQLEEDIVSARRSDLYSELSRESRLAAEFKATRCQHK 609

Db 508 LQHKNAEYQRAVDHEADKKNLENVNSLKQLEBDLKKQNOQI9TE-----KVNDLQ 563

Qy 610 LKAKDQGPVEGVAYLKEKINAEQOLKIQ-----ELOEK--LEKAKARERLELEK 660

Db 564 LDETALARTESDPAARLARKTOAESSKOIQLESNNMDLQDKCLLETALKEKEFINL 623

Qy 661 QNRDSSSEGTAKULVEABERHSLNKNVYKLETERENRNLKODIOTKSQOIQOMADKIL 720

Db 624 QSALESE---RRDTGSEIINDIQGRI CGLEEDLKGGKILLAKVELBKQLOERFPD-L 679

Qy 721 ELEEGHRAOVSQAQ--HLEVLAKQK--OHYEKIKVLN-NOIKKDL--ADKETLENNMOR 774

Db 680 EKEKSNMEIDMTYQKVIQSLQEBEAHKATKARLADKNKYISIEAASEAKMEK 739

Qy 775 HEEBAHEKGI--LSEQKAMINAMDSKIRLEBQRYVELSANTLANNSLFTQNNKAQ 831

Db 740 LLEERTLKQYENILLEAEKCSLLDCLOKSOOKINEL-----LQK 782

Qy 832 EEMISELAQKFYLETQAGKLEAQNRLKEBQLEKISHODSDKRLLELTRLEVSLEH 891

Db 783 DVLNEDVNRNLTIKIETQKCCLTQNDLAKQTOOVNTLAKSEK-QLQOENNHLMEMQNL 841

Qy 892 BEQKLEKQLTLEQLSOERESQTLTALOARAALESQLOAKTELETT--AAEBEI 948

Db 842 EKQNAELKREKRDADQKKELQDQLEAEOYSTLYKTVREIKECCEKTKLQKLEQKK 901

Qy 949 QALTARDEIQKPPALANSCTVITDLEQNLQTLNDAELNNOFYLISKQDEASGAND 1008

Db 902 QEIODERISIAQLE-----ITLTADSQBLARSTAEBOYSDBLEKTKMKE----- 947

Qy 1009 EIVOLRSEVDNLRREITEREMQTSQKOTMEALKTCTMLEBOVNDLEALNDELIEKQ 1068

Db 948 --LEIKEMARKQKQETEDATIASLEETNRILTSDVANLAN--EKEELNNKLQDVOEQ 1002

Qy 1069 WEAMRSVLQDE-----KSQECRAVEIQRMLDTEKOSBARADQITSRQVVELAVEN 1121

Db 1003 ---LSRLKDEEISAALIAQFE-----KOLTERTLKTQAVVKL----- 1038

Qy 1122 HKQELLALQQAQKQGLKXBSLSDKLNDEKKAAMLEMNARSLOOKLETREBELKORLEE 1181

Db 1039 --AEINRKEEYK-----KANDTVARK--EKENRKLHNEIKSERE--KLQO 1080

Qy 1182 QAKLQOQMDLQKNHIFRLTQ--GLQALDRADLKTERSDLEVOLENIOVLY----- 1231


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Db      1003 ----LSRLDEBISAIAKAQFE-----KQLTERLTQTQAVNKL----- 1038
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Db      1039 --AEIWRKREPVK-----RGNDDVRRK--EKENRLHMLSEERE--KLTYQ 1080
Oy      1182 QAKLQOQMLQKNHIFRLTQ---GLQELDRADILKTERSDLEVOLENIQVLY----- 1231
Db      1081 MKTYQKEIEMQALIEESQIRLEQMTDSKD-----SDIEQARSQALHIGLSDSS 1134
Oy      1232 -----SHEKVMETIS-----OQTKLIDELQAKMDQPAKKKGLFSRKKEDPA 1275
Db      1135 IGSQPDADBADDFPSPRLGMLSLPVNNTKKFGVKKYIVSSKKILFYFSEODKEQS 1194
Oy      1276 LPTQV-----PLQYNELKLALEKKAQAELEALQKTRIELRSAREBAHRKAT 1325
Db      1195 NPYWVLIDIDLFFHVRPVLTQTDVVRADAKELPRIFQI----- 1230
Oy      1326 DHPHPTPATARQOIMSAIVRSPEHQPSAMSLAPPSSRRKESSTP---EFSRRLKE 1381
Db      1231 -----LYANEGSSKKQOEFPVPEVGEKSNYICH 1258
Oy      1382 RMHINI PHRENVGLNMRATKCAVCLDTVHFGQASCKLECCQVGCPEXC 1429
Db      1259 KGHFIPTLYHF-----PTNCEACMKPMLMHMFPRPALCR-RCHIKC 1300

RESULT 13
US-09-916-204-4
; Sequence 4, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-916-204-4

Query Match      11.2%; Score 1173; DB 4; Length 251;
Best Local Similarity 90.0%; Pred. No. 2.9e-53;
Matches 226; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Oy      1 MLKRYGARNPLDGAAPIASRASRLNLFPGKPPMTQOQMSPLSRGLDALTFLVFE 60
Db      1 MLKRYGARNPSEASAPPIASRASRLNLFQGRPLMTQOQMSALSREGVLDLFLVLE 60
Oy      61 ECSOPALMKIKHVSFVRKYSDTIAELRELQPSVRDEVSLSVCGHFAEYQVVRKATG 120
Db      61 ECSOPALMKIKHVSFVRKYSDTIAELRELQPSVRDEVSLSVCGHFAEYQVVRKATG 120
Oy      121 DIYAMVKKKKALLAQBQVSPFEERNTLSRSTSPMIPOLQYAFQDKNHLYLMEYOPGG 180
Db      121 DVIAMKIMKKAALRAQEQVSPFEERNTLSQSTSPMIPOLQYAFQDKNHLYLMEYOPGG 180
Oy      181 DLSLNRYPQDLDENLQFYLAELILAVSHVHMGVYHRDIKENILVDRTHIKLVDF 240
Db      181 DLSLNRYPQDLDENLQFYLAELILAVSHVHMGVYHRDIKENILVDRTHIKLVDF 240
Oy      241 GSAAMNSNM 251

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Db      241 GSAAMNSNM 251

RESULT 14
US-10-282-048-4
; Sequence 4, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-282-048-4

Query Match      11.2%; Score 1173; DB 4; Length 251;
Best Local Similarity 89.6%; Pred. No. 4.1e-53;
Matches 225; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

Oy      1 MLKRYGARNPLDGAAPIASRASRLNLFPGKPPMTQOQMSPLSRGLDALTFLVFE 60
Db      1 MLKRYGARNPSEASAPPIASRASRLNLFQGRPLMTQOQMSALSREGVLDLFLVLE 60
Oy      61 ECSOPALMKIKHVSFVRKYSDTIAELRELQPSVRDEVSLSVCGHFAEYQVVRKATG 120
Db      61 ECSOPALMKIKHVSFVRKYSDTIAELRELQPSVRDEVSLSVCGHFAEYQVVRKATG 120
Oy      121 DIYAMVKKKKALLAQBQVSPFEERNTLSRSTSPMIPOLQYAFQDKNHLYLMEYOPGG 180
Db      121 DVIAMKIMKKAALRAQEQVSPFEERNTLSQSTSPMIPOLQYAFQDKNHLYLMEYOPGG 180
Oy      181 DLSLNRYPQDLDENLQFYLAELILAVSHVHMGVYHRDIKENILVDRTHIKLVDF 240
Db      181 DLSLNRYPQDLDENLQFYLAELILAVSHVHMGVYHRDIKENILVDRTHIKLVDF 240
Oy      241 GSAAMNSNM 251

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Db 1 MLKFKYGVNRNPPPEASASEPTIASRASRLNLFQCKPPLMTQOMKALSREGMLDALFALFE 60
QY 61 ECSQPALMKIKHVSNTFRKYSDTIAELOEPSAKDFEVRSLVCGHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSNTFRKYSDTIAELOEPSAKDFEVRSLVCGHFAEVQVVRKATG 120
QY 121 DIYAMKVMKKKALLAOBOVSFFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYOPGG 180
Db 121 DVTAMKIMKKKALLAOBOVSFFEEERNILSRSTSPWIPOLQYAFODKNHLYLMEYOPGG 180
QY 181 DLSLNLRYEDQDENLQFYLAELILAVSHVLMGVHRDIKPENILVDRGTGHIKLVDF 240
Db 181 DFLSLNLRYEDQDENLQFYLAELILAVSHVLMGVHRDIKPENILVDRGTGHIKLVDF 240
QY 241 GSAKKNNSNM 251
Db 241 GSAKKNNSNM 251

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OM protein - protein search, using SW model

Run on: February 27, 2005, 13:45:16 ; Search time 203 Seconds

(Without alignments)
3317.613 Million cell updates/sec

Title: US-10-017-216-2

Perfect score: 10490
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Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	10480	100.0	2053	14	US-10-325-430-12
3	10490	100.0	2053	16	US-10-757-262-52
4	10032.5	95.6	2054	15	US-10-415-011-21
5	10022.5	95.5	2054	13	US-10-028-946-2
6	10011	95.4	2055	16	US-10-618-941-67
7	10007	95.4	2066	11	US-09-964-956-9
8	10007	95.4	2066	15	US-10-262-511-14
9	10005	95.4	2053	11	US-09-964-956-11
10	10005	95.4	2053	15	US-10-262-511-2
11	9487.5	90.4	2055	13	US-10-017-216-4
12	9487.5	90.4	1958	13	US-10-028-946-4
13	7717.5	73.6	1641	11	US-09-964-956-40

14	7717.5	73.6	1641	13	US-10-017-216-5	Sequence 5, Appli
15	7491.5	71.4	1597	11	US-09-964-956-41	Sequence 41, Appli
16	7491.5	71.4	1597	11	US-10-017-216-6	Sequence 6, Appli
17	6745.5	64.3	1441	15	US-10-412-897-3	Sequence 3, Appli
18	6223.5	59.3	1286	11	US-09-964-956-38	Sequence 38, Appli
19	6223.5	59.3	1286	13	US-10-017-216-7	Sequence 7, Appli
20	4718.5	45.0	999	15	US-10-276-774-1487	Sequence 1487, Ap
21	4519.5	43.1	940	11	US-09-964-956-39	Sequence 39, Appli
22	4249.5	40.5	883	11	US-09-964-956-37	Sequence 37, Appli
23	4101	39.1	847	15	US-10-262-511-8	Sequence 8, Appli
24	4005.5	38.2	832	15	US-10-262-511-6	Sequence 6, Appli
25	3155	30.1	623	15	US-10-262-511-4	Sequence 4, Appli
26	2910	27.7	623	15	US-10-262-511-10	Sequence 10, Appli
27	2892.5	27.6	638	15	US-10-262-511-12	Sequence 12, Appli
28	2430	23.2	497	9	US-09-804-471A-2	Sequence 2, Appli
29	2430	23.2	497	14	US-10-238-709-2	Sequence 2, Appli
30	2430	23.2	497	15	US-10-724-594-2	Sequence 2, Appli
31	2425	23.1	497	15	US-10-311-034-7	Sequence 7, Appli
32	2165.5	20.6	494	9	US-09-804-471A-4	Sequence 4, Appli
33	2165.5	20.6	494	14	US-10-238-709-4	Sequence 4, Appli
34	2165.5	20.6	494	15	US-10-724-594-4	Sequence 4, Appli
35	1700	16.2	373	15	US-10-120-835-42	Sequence 42, Appli
36	1645	15.7	319	15	US-10-412-897-2	Sequence 2, Appli
37	1446	13.8	1770	15	US-10-433-794-19	Sequence 19, Appli
38	1421.5	13.6	1719	15	US-10-288-798-2	Sequence 2, Appli
39	1421.5	13.6	1719	15	US-10-362-892-2	Sequence 2, Appli
40	1400	13.3	1738	15	US-10-210-130-100	Sequence 100, App
41	1399.5	13.3	1664	15	US-10-210-130-102	Sequence 102, App
42	1383.5	13.2	1711	17	US-10-781-581-206	Sequence 206, App
43	1382.5	13.2	1711	9	US-09-771-161A-219	Sequence 219, App
44	1382.5	13.2	1711	9	US-09-771-161A-220	Sequence 220, App
45	1382.5	13.2	1711	15	US-10-399-225-10	Sequence 10, Appli

ALIGNMENTS

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RESULT 1
US-10-017-216-2
; Sequence 2, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMAN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1et Human Myotonic Dystrophy Type Pro
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017,216
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-216-2

Query Match      100.0%; Score 10490; DB 13; Length 2053;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2053; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 MKPKFGARNPLDAGAAEPIASRA SRLNFQGKPEPMTQOMSPLSREGIDALFVLE 60
QY      61 ECGSGLMKIKIVSNFVKYSSTIAELQELQPSADFEVRSIVGCGHRAEVOVREKATG 120
DB      61 ECGSGLMKIKIVSNFVKYSSTIAELQELQPSADFEVRSIVGCGHRAEVOVREKATG 120
QY      121 DIYANKWKKKALLAQEQVSPFEERNTLSRSTSPWIPOLQYAFQDKNHLVMEBYOPGG 180
DB      121 DIYANKWKKKALLAQEQVSPFEERNTLSRSTSPWIPOLQYAFQDKNHLVMEBYOPGG 180
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181 DLSLNLRYEDODENT.IOPYLAELLAVHSVHLMGVYHRDIKRENTLVDRGHTILVDPF 240
241 GSAAKNNSNMVNAKLPIGTDPYMAPEVLTVNMGDKGTGYGLDCDMMWVGVIAEM1YGR 300
241 GSAAKNNSNMVNAKLPIGTDPYMAPEVLTVNMGDKGTGYGLDCDMMWVGVIAEM1YGR 300
301 SPPAEGTSARTFNINNFQRFKFPDDPKYSSDFLLIOSLCCGQKRLKTBGLCCHPFP 360
301 SPPAEGTSARTFNINNFQRFKFPDDPKYSSDFLLIOSLCCGQKRLKTBGLCCHPFP 360
361 SKIDMNNINSPPEFVPTLKSDDDTSNPDEPEKNSVWSSPCOLSPSGSGEELPVVGS 420
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541 D1REOSRKLQETKEOEYQAOVEEMRLMMNQLLEEDLVASARRSDLYRSELRESRLAEEBK 600
541 D1REOSRKLQETKEOEYQAOVEEMRLMMNQLLEEDLVASARRSDLYRSELRESRLAEEBK 600
601 RRATECOHKLKRAKODGKEVEGYAKLEKINAEOQLKIOLEKLEKAKERARELEKL 660
601 RRATECOHKLKRAKODGKEVEGYAKLEKINAEOQLKIOLEKLEKAKERARELEKL 660
661 QNRBESSEIGIRKKLVAEERRHSLLENKVRLEMTMERENRLKODIOTKSQOIQANADKL 720
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721 ELBEEKREAOVSAOHLVEHLKQKEQHYEEKIKVLDNQIKKDLADKTELLENMQRHEEBAH 780
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781 EKGKILISEQKAMINAMDSKIRSLSEQRIVELSEANKLAANSSLEFQNMKAQOEEMISELQ 840
841 QKPYLETQKLEBAQNRKLEBOLEKISHODHSDKNNLELETRLRVSLHEEOKLELR 900
841 QKPYLETQKLEBAQNRKLEBOLEKISHODHSDKNNLELETRLRVSLHEEOKLELR 900
901 QUTELQLSLOERESQUTALQAARAALESOLROAKTELEETABAEEIQALTARDEIOR 960
901 QUTELQLSLOERESQUTALQAARAALESOLROAKTELEETABAEEIQALTARDEIOR 960
961 KFDALRNSCTVITLDEEQLNQLTEDNAELNNONFYLSKQLEDAAGANDEIVOLRSEVDL 1020
961 KFDALRNSCTVITLDEEQLNQLTEDNAELNNONFYLSKQLEDAAGANDEIVOLRSEVDL 1020
1021 REEITEREMQULTSOQOTMEALKTCTCMLEEOVMDEALNDELLEKROEAMRSVIGDEX 1080
1021 REEITEREMQULTSOQOTMEALKTCTCMLEEOVMDEALNDELLEKROEAMRSVIGDEX 1080
1081 SOFECRVRELQMLDTEKOSRARADQRTESRQVVELAVKEHKAETIALAQALKEQKLYA 1140
1081 SOFECRVRELQMLDTEKOSRARADQRTESRQVVELAVKEHKAETIALAQALKEQKLYA 1140
1141 ELSLSQKLANDLEKHAMLENNANSLQOKLETERBELKORLLEBOAKLQOQWDLQKNHIFRLT 1200
1141 ELSLSQKLANDLEKHAMLENNANSLQOKLETERBELKORLLEBOAKLQOQWDLQKNHIFRLT 1200
1201 OGLQELADRADLLKTERSPLLEYOLENIOVLVSHKVKMGEGTSOOTKLDLPIQAKKDQPA 1260
1201 OGLQELADRADLLKTERSPLLEYOLENIOVLVSHKVKMGEGTSOOTKLDLPIQAKKDQPA 1260

1261 KKKKGLFSRRKEDPALPTQVPLQYNELKLALEKEKARCAELEBEALOKTRIELRSAREBA 1320
1261 KKKKGLFSRRKEDPALPTQVPLQYNELKLALEKEKARCAELEBEALOKTRIELRSAREBA 1320
1321 HRKATDHPHPSPTPATARQOIJAMSAIVRSBHOPSAMSLAPSSRRKESSTEEPSRLK 1380
1321 HRKATDHPHPSPTPATARQOIJAMSAIVRSBHOPSAMSLAPSSRRKESSTEEPSRLK 1380
1381 ERMHNINIPHRFVNGAMNATKCAVCLDLYHFERQASKCLEQWCHPCKSTCLPATCGLP 1440
1381 ERMHNINIPHRFVNGAMNATKCAVCLDLYHFERQASKCLEQWCHPCKSTCLPATCGLP 1440
1441 AEYATHFTEAPCRDKMNSPGLOTKEPSSSLHLEGMMKYPNNKRQOQGWDRKYIVLESGK 1500
1441 AEYATHFTEAPCRDKMNSPGLOTKEPSSSLHLEGMMKYPNNKRQOQGWDRKYIVLESGK 1500
1501 VLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELIANTAKAKABADAKLGNLSL 1560
1501 VLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELIANTAKAKABADAKLGNLSL 1560
1561 KLEGGDRLLDMNCTLPFSQVYVVLVTEBGLYALNTVKNSLTHVPGLGAVFOIYIITDLEKL 1620
1561 KLEGGDRLLDMNCTLPFSQVYVVLVTEBGLYALNTVKNSLTHVPGLGAVFOIYIITDLEKL 1620
1621 LMAGEERBALCLVDYKVKYOSLAQSHLPAOPDISPNIPEAVVGCHLFGAGKIENGCLICA 1680
1621 LMAGEERBALCLVDYKVKYOSLAQSHLPAOPDISPNIPEAVVGCHLFGAGKIENGCLICA 1680
1681 AMPSKRVILRYNENLSKYCIRKEIETSEPCGCIHFTNYSILIGTNKFEYIDMKQYTLLEEF 1740
1681 AMPSKRVILRYNENLSKYCIRKEIETSEPCGCIHFTNYSILIGTNKFEYIDMKQYTLLEEF 1740
1741 LDKNHSIAPAVEASNSFPVSIYVUNVAGOREEYLLCFHEFGVFNUSYGRSRSTDCLK 1800
1741 LDKNHSIAPAVEASNSFPVSIYVUNVAGOREEYLLCFHEFGVFNUSYGRSRSTDCLK 1800
1801 WSRLLPAAVREPYLFVTHFNLSLEVIEIOANSSAGTTPARAYLDIPNPRYLGPALISSGAY 1860
1801 WSRLLPAAVREPYLFVTHFNLSLEVIEIOANSSAGTTPARAYLDIPNPRYLGPALISSGAY 1860
1861 IASSYODKLRYVICCKNLVKSGETEHRGPSTSRSSPNKRGPPYNEHITYKRVASSPAP 1920
1861 IASSYODKLRYVICCKNLVKSGETEHRGPSTSRSSPNKRGPPYNEHITYKRVASSPAP 1920
1921 BGGSHPRESTPHRRRBRBTELRDPSRGPRLERKSGRMLSTRRESPGRLPFDSSRG 1980
1921 BGGSHPRESTPHRRRBRBTELRDPSRGPRLERKSGRMLSTRRESPGRLPFDSSRG 1980
1981 RLPAGAVRTPLSQVKNKGOSASQVFTVNTVTVYVDMNKKLDNLPANWSVLRIIQLNGEIR 2040
1981 RLPAGAVRTPLSQVKNKGOSASQVFTVNTVTVYVDMNKKLDNLPANWSVLRIIQLNGEIR 2040
2041 QOVEKSVLRTDYC 2053
2041 QOVEKSVLRTDYC 2053

RESULT 2
US-10-325-430-12
Sequence 12, Application US/10325430
Publication No. US20030153525A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Rosenfeld, Julie Beth
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
FILE REFERENCE: MP101-294PIBM
CURRENT APPLICATION NUMBER: US/10/325,430
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/341,953
PRIOR FILING DATE: 2001-12-19

; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 2053
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-325-430-12

Query Match 100.0%; Score 10490; DB 14; Length 2053;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matched 2053; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFKYGAANPLDAGAAEPPIASPASRLNFFQGGPPMTQOQMSPLSRREGILDALFVLE 60
 DB 1 MKFKYGAANPLDAGAAEPPIASPASRLNFFQGGPPMTQOQMSPLSRREGILDALFVLE 60
 QY 61 ECSQAPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVSILVGCCHPAFVQVVERKATG 120
 DB 61 ECSQAPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVSILVGCCHPAFVQVVERKATG 120
 QY 121 DIYAMVMMKKKALLAQEOVSFFEEERNILSRSTSPWIPOLQYAFODKXNLYLMEEQPG 180
 DB 121 DIYAMVMMKKKALLAQEOVSFFEEERNILSRSTSPWIPOLQYAFODKXNLYLMEEQPG 180
 QY 181 DLLSLNRYEDOLDENLYQFYLAELILAVSHVLMGVYHRDIKPENILVDRTGHIKLVDP 240
 DB 181 DLLSLNRYEDOLDENLYQFYLAELILAVSHVLMGVYHRDIKPENILVDRTGHIKLVDP 240
 QY 241 GSAAKNNSNMVNAKLPIGTPOYMAPEVLTVNNGDGKGTGLDCDMMSVGVIAEM1YGR 300
 DB 241 GSAAKNNSNMVNAKLPIGTPOYMAPEVLTVNNGDGKGTGLDCDMMSVGVIAEM1YGR 300
 QY 301 SPPAESTARTPNINNFQPLKFPDDPKVSSPDLIQLSLCGQKERLKFBEELCHPFP 360
 DB 301 SPPAESTARTPNINNFQPLKFPDDPKVSSPDLIQLSLCGQKERLKFBEELCHPFP 360
 QY 361 SKIDMNNINSPPEFVTLKSDDDTSNFPBPKNSVSSPCOLSPSGSGEELPVGVS 420
 DB 361 SKIDMNNINSPPEFVTLKSDDDTSNFPBPKNSVSSPCOLSPSGSGEELPVGVS 420
 QY 421 YKALGILGRSESVSGLDSPAKTSMKKLLIKSKXELQSDQCHKMEQEMTRLHRRVS 480
 DB 421 YKALGILGRSESVSGLDSPAKTSMKKLLIKSKXELQSDQCHKMEQEMTRLHRRVS 480
 QY 481 EYEAVALSQEVELKASETORSLLEODLATYITECSSLKSLBEAPRMEVQOEDKALQILH 540
 DB 481 EYEAVALSQEVELKASETORSLLEODLATYITECSSLKSLBEAPRMEVQOEDKALQILH 540
 QY 541 DREOSRKLQELKEOEYQAOVEEMRLMMNOLEEDLVSARRSDLYSESLRESRLAEEFK 600
 DB 541 DREOSRKLQELKEOEYQAOVEEMRLMMNOLEEDLVSARRSDLYSESLRESRLAEEFK 600
 QY 601 RKATECOHLLAKQOGKPEVEGYALTEKINAEQOLKIOELQEKLEKAKERARELEK 660
 DB 601 RKATECOHLLAKQOGKPEVEGYALTEKINAEQOLKIOELQEKLEKAKERARELEK 660
 QY 661 QNRBDSSEGIKKLVAEERRHSLKLVKRLLETMERENRLKDDIOTKSOQIQOAMDKLL 720
 DB 661 QNRBDSSEGIKKLVAEERRHSLKLVKRLLETMERENRLKDDIOTKSOQIQOAMDKLL 720
 QY 721 ELBEKREAOVSOHLEVHLKQKOEYEEKIKVLDQIKKDLADKTELNNMORHEEAAH 780
 DB 721 ELBEKREAOVSOHLEVHLKQKOEYEEKIKVLDQIKKDLADKTELNNMORHEEAAH 780
 QY 781 EKGKILSEQKAMINAMDSKIRSLERIVELSEANKLAANSJLFTQNMKAQOEEM1SELNO 840
 DB 781 EKGKILSEQKAMINAMDSKIRSLERIVELSEANKLAANSJLFTQNMKAQOEEM1SELNO 840
 QY 841 QKFYLETQAGKLEAQRKLEBOLEKISHODHSDXNLLLETFLRLSVSLHEHEOKLELR 900
 DB 841 QKFYLETQAGKLEAQRKLEBOLEKISHODHSDXNLLLETFLRLSVSLHEHEOKLELR 900
 QY 901 QLTTELQSLQERESQUTALQAARALLESQLRQAKTELETTAAAESEIQALTARHDEIQR 960

DB 901 QLTTELQSLQERESQUTALQAARALLESQLRQAKTELETTAAAESEIQALTARHDEIQR 960
 QY 961 KFDALRNSCTVTIDLEQNLQUTEDNAELANNQFYLISKQLDASGANDBIYOLRSVDM 1020
 DB 961 KFDALRNSCTVTIDLEQNLQUTEDNAELANNQFYLISKQLDASGANDBIYOLRSVDM 1020
 QY 1021 RREITEREMQLTSSQOTMEALKTTCCTMLEEQVMDLEANDLEBEKROWEAMRSVLDGDK 1080
 DB 1021 RREITEREMQLTSSQOTMEALKTTCCTMLEEQVMDLEANDLEBEKROWEAMRSVLDGDK 1080
 QY 1081 SQPECRVRELQMLDTEKOSRARADQRTESQVVELAVKEKABILALQALKEQKXKA 1140
 DB 1081 SQPECRVRELQMLDTEKOSRARADQRTESQVVELAVKEKABILALQALKEQKXKA 1140
 QY 1141 ESLSDKLANDLEKXAMLENNASLOQKLETEBELQRLLEBOAKILOQMDLQXNHFRLT 1200
 DB 1141 ESLSDKLANDLEKXAMLENNASLOQKLETEBELQRLLEBOAKILOQMDLQXNHFRLT 1200
 QY 1201 OGLQELADRADILKTERSDLEYQLENIOVLYSHKRYKMGTTISQOTKLDPLQAKMDQPA 1260
 DB 1201 OGLQELADRADILKTERSDLEYQLENIOVLYSHKRYKMGTTISQOTKLDPLQAKMDQPA 1260
 QY 1261 KKKKGLFSRKKEDPALPTQVPLQVNEKLALKEKARCALEBEALQKTRIELRSAREEA 1320
 DB 1261 KKKKGLFSRKKEDPALPTQVPLQVNEKLALKEKARCALEBEALQKTRIELRSAREEA 1320
 QY 1321 HRKATDHPHSTPATARQOIAWSAIVRSBEHOPSAWSLIAFPSSRRKESSTPEESRRLK 1380
 DB 1321 HRKATDHPHSTPATARQOIAWSAIVRSBEHOPSAWSLIAFPSSRRKESSTPEESRRLK 1380
 QY 1381 ERMHNHPIRPFVNGIMRA TKCAVCLDPTVHFRQASKCLEQVMCHPKSTCLPATCGLP 1440
 DB 1381 ERMHNHPIRPFVNGIMRA TKCAVCLDPTVHFRQASKCLEQVMCHPKSTCLPATCGLP 1440
 QY 1441 AEYATHTFEAFCRDKMNSFGLOTKEPSSSLHLEGMMKPRANKRQCGQMDRKYIVLEGSK 1500
 DB 1441 AEYATHTFEAFCRDKMNSFGLOTKEPSSSLHLEGMMKPRANKRQCGQMDRKYIVLEGSK 1500
 QY 1501 VLIYNEAREAGQREVEBEELCPDGDVSIHGAVASBELANTAKAEKEADAKLGNSTLL 1560
 DB 1501 VLIYNEAREAGQREVEBEELCPDGDVSIHGAVASBELANTAKAEKEADAKLGNSTLL 1560
 QY 1561 KLEGDRLDMNCTLPSPQVVLVGTBEGLYALNVKNSLTHVPGIYAVQIYIIMOLEK 1620
 DB 1561 KLEGDRLDMNCTLPSPQVVLVGTBEGLYALNVKNSLTHVPGIYAVQIYIIMOLEK 1620
 QY 1621 LMIAGEERALCLVDYKVKQSLAQSHLPAQPDISPNIPEAVNGCHLFGAGKILENGLCICA 1680
 DB 1621 LMIAGEERALCLVDYKVKQSLAQSHLPAQPDISPNIPEAVNGCHLFGAGKILENGLCICA 1680
 QY 1681 AMPSKVILIRYENELSKYCIKRIEITSEBPCSIHFTNYSILIGTKFYEDIMKOYTLLEEF 1740
 DB 1681 AMPSKVILIRYENELSKYCIKRIEITSEBPCSIHFTNYSILIGTKFYEDIMKOYTLLEEF 1740
 QY 1741 LDKNDHSLAPAVFAASSNFPVSIYVNSAGOREEYLLCFHEFGVYVSGYGRSSTDCLK 1800
 DB 1741 LDKNDHSLAPAVFAASSNFPVSIYVNSAGOREEYLLCFHEFGVYVSGYGRSSTDCLK 1800
 QY 1801 WSRPLAFAYREPYLFVTHFNLSLEYEIQARSASGATPARAYDIDINPRYLGPAISSGAY 1860
 DB 1801 WSRPLAFAYREPYLFVTHFNLSLEYEIQARSASGATPARAYDIDINPRYLGPAISSGAY 1860
 QY 1861 IASSYQDKLAVICCKGNLVKSGTEHHRGPSTSRSSPNKRGPTYNEHITKXVASSPAP 1920
 DB 1861 IASSYQDKLAVICCKGNLVKSGTEHHRGPSTSRSSPNKRGPTYNEHITKXVASSPAP 1920
 QY 1921 EGPSPHREPESTHRRREGTELRKDXSPGRPLERKSGRM1STREBSRGLFEDSSRG 1980
 DB 1921 EGPSPHREPESTHRRREGTELRKDXSPGRPLERKSGRM1STREBSRGLFEDSSRG 1980
 QY 1981 RLPAGAVPTPLSQVKKGRGQASQVFTVTVYVYMNKLDLPLAMWSVLRIIQLANGEIR 2040

Db 1981 RLPAGAVRPLSQVNGRGSGASQVFTVNTVYTYDMNKKLDNLPANWSVLRTIQNGEIR 2040
QY 2041 QOVERSVLRDYC 2053
Db 2041 QOVERSVLRDYC 2053

RESULT 3
US-10-757-262-52
Sequence 52, Application US/10757262
Publication No. US20040197825A1
GENERAL INFORMATION:
APPLICANT: Karicheti, Venkateswarlu
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Eliasof, Scott D
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
FILE REFERENCE: MP103-007P1RNMNM
CURRENT APPLICATION NUMBER: US/10/757,262
PRIOR FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 60/440,318
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/444,783
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: US 60/457,901
PRIOR FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/468,775
PRIOR FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US 60/471,614
PRIOR FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: US 60/478,742
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 60/488,529
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/491,156
PRIOR FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US 60/499,594
PRIOR FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US 60/506,332
PRIOR FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 2053
TYPE: PRT
ORGANISM: Homo sapiens
US-10-757-262-52

Query Match 100.0%; Score 10490; DB 16; Length 2053;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2053; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 DLSLNLRYEDQDLDNLIQFYLAELILAVHSVHLMGVYHRDIKPEINILVDRGTGHIKLVDF 240
QY 241 GSAAKNSNKNVNAKLPIGTPDYNAPEVLTWNNGDGKGYGLDCDMSGVAYAYEMITGR 300
Db 241 GSAAKNSNKNVNAKLPIGTPDYNAPEVLTWNNGDGKGYGLDCDMSGVAYAYEMITGR 300
QY 301 SPFAAGTSARTFNNIMNFQRLKFPDDPKVSSDFLDLIQSLICQKRLKEGLCCHPFF 360
Db 301 SPFAAGTSARTFNNIMNFQRLKFPDDPKVSSDFLDLIQSLICQKRLKEGLCCHPFF 360
QY 361 SKIDNNIRNSPPVPVPLTKSDDDTSNDEPEKNSWSSPCQSPSGFSEBELPFGFS 420
Db 361 SKIDNNIRNSPPVPVPLTKSDDDTSNDEPEKNSWSSPCQSPSGFSEBELPFGFS 420
QY 421 YSKALGILGRSBSVSGDPSAKTSMKSKLLIKSKELQDSQDKCHKKEQENTRLHRYS 480
Db 421 YSKALGILGRSBSVSGDPSAKTSMKSKLLIKSKELQDSQDKCHKKEQENTRLHRYS 480
QY 481 EYEAVLSQYVELKASEFORSLEODLATYITTECSLSKRSLEQARMEVSOEDDKALQILH 540
Db 481 EYEAVLSQYVELKASEFORSLEODLATYITTECSLSKRSLEQARMEVSOEDDKALQILH 540
QY 541 DIREQSRLOEIKGOEYQAOYEEMRLMNNOLEEDLVASRRSDIYESELRESRLAAEFK 600
Db 541 DIREQSRLOEIKGOEYQAOYEEMRLMNNOLEEDLVASRRSDIYESELRESRLAAEFK 600
QY 601 RKATECOHKLKANDOGKPEVEGYAKLEKINAEOOLKIQELOEKLKAKAKARELEKL 660
Db 601 RKATECOHKLKANDOGKPEVEGYAKLEKINAEOOLKIQELOEKLKAKAKARELEKL 660
QY 661 QNRDSSGIRKKI VEAERHRHSLENYKYLETERRBNRLKDIQYKSQOIQQMADKIL 720
Db 661 QNRDSSGIRKKI VEAERHRHSLENYKYLETERRBNRLKDIQYKSQOIQQMADKIL 720
QY 721 ELEEKHRAQVSAOHLVHLKQKQYHEEKIKVLDNOIKDOLAKETLENNMOHREBAH 780
Db 721 ELEEKHRAQVSAOHLVHLKQKQYHEEKIKVLDNOIKDOLAKETLENNMOHREBAH 780
QY 781 EKGKILSEQKAMINAMDSKIRSLRQIVLSEANKLANSLSFTORMKQOZEMISELRO 840
Db 781 EKGKILSEQKAMINAMDSKIRSLRQIVLSEANKLANSLSFTORMKQOZEMISELRO 840
QY 841 OKFYLETQAGLEQONKRLBEOLEKISHODSDPNRLLELTRRVSLEHEBKLELR 900
Db 841 OKFYLETQAGLEQONKRLBEOLEKISHODSDPNRLLELTRRVSLEHEBKLELR 900
QY 901 QUTLEQSLQERESQUTLQAARALSESQRLAKTELEETTAEBEETIOALTARDEIOR 960
Db 901 QUTLEQSLQERESQUTLQAARALSESQRLAKTELEETTAEBEETIOALTARDEIOR 960
QY 961 KFDALRNSCTVITDLEQNLQUTEDNAELNNOIFYLSKQULDEASGANDEIVQURSEVDHL 1020
Db 961 KFDALRNSCTVITDLEQNLQUTEDNAELNNOIFYLSKQULDEASGANDEIVQURSEVDHL 1020
QY 1021 RREITEREMOITSKOMTEALKTTCTMLEBOWMDLELNNELLEKEQWAMSVLGDEK 1080
Db 1021 RREITEREMOITSKOMTEALKTTCTMLEBOWMDLELNNELLEKEQWAMSVLGDEK 1080
QY 1081 SOPECRVRELORMDITEKOSRARADQRTESROVVELAVENHKAETIALQALKEQCLKA 1140
Db 1081 SOPECRVRELORMDITEKOSRARADQRTESROVVELAVENHKAETIALQALKEQCLKA 1140
QY 1141 ESLSDKINDLEKGMALNNARSLOQKLETERELKORLLEBEOAKLQQQMDLQKXHFRLT 1200
Db 1141 ESLSDKINDLEKGMALNNARSLOQKLETERELKORLLEBEOAKLQQQMDLQKXHFRLT 1200
QY 1201 QGLQDALDRADILKTERSDILEYOLENIQVLYSEKXVMESTISOQTKLIDFLQAKXDPA 1260
Db 1201 QGLQDALDRADILKTERSDILEYOLENIQVLYSEKXVMESTISOQTKLIDFLQAKXDPA 1260
QY 1261 KKKKGLFSRKEDPALPTQVPLQYNELKALAEKAKCALEBALQOTRIELASAREEA 1320
Db 1261 KKKKGLFSRKEDPALPTQVPLQYNELKALAEKAKCALEBALQOTRIELASAREEA 1320

Db 1261 KKKKGLFSRRKEDBPLTQVPLQYNELKALKEKAKCAELEBALTQTRIELSAREBEA 1320
 Qy 1321 HRAKTHPHBSTATATAOQIAMSAYSPBHOPSAMSLAPPSRRRESTPPEFSRLK 1380
 Db 1321 HRAKTHPHBSTATATAOQIAMSAYSPBHOPSAMSLAPPSRRRESTPPEFSRLK 1380
 Qy 1381 ERMHNNI PHRFNVLNMRATKCAVCLDTVHFGROASCLCQWCHPKSTCPLPATGCLP 1440
 Db 1381 ERMHNNI PHRFNVLNMRATKCAVCLDTVHFGROASCLCQWCHPKSTCPLPATGCLP 1440
 Qy 1441 AEYATHTFAFCBDRKONS PGLQTKBPSSSLHLEGMKVPNNKRGQGGWDRKXIVLESGK 1500
 Db 1441 AEYATHTFAFCBDRKONS PGLQTKBPSSSLHLEGMKVPNNKRGQGGWDRKXIVLESGK 1500
 Qy 1501 VLLYDNEARAGRPVEEFELCLPDGVSTHGAVASSELANTAKAEQAEADALUGSL 1560
 Db 1501 VLLYDNEARAGRPVEEFELCLPDGVSTHGAVASSELANTAKAEQAEADALUGSL 1560
 Qy 1561 KLEGBDRLDMMCTLPFSDQVVLVGTBEGLYALNVLKSLTHVPGIGAVFOIYIIXDLKEL 1620
 Db 1561 KLEGBDRLDMMCTLPFSDQVVLVGTBEGLYALNVLKSLTHVPGIGAVFOIYIIXDLKEL 1620
 Qy 1621 LMIAGEERALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAUVKGCHLFGAKIENGLCICA 1680
 Db 1621 LMIAGEERALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAUVKGCHLFGAKIENGLCICA 1680
 Qy 1681 AMPSKVVILRYNNELSTYCIKKEIETSEPCSHFTYVSTLIGTNKYEYEDMKQYTLLEEF 1740
 Db 1681 AMPSKVVILRYNNELSTYCIKKEIETSEPCSHFTYVSTLIGTNKYEYEDMKQYTLLEEF 1740
 Qy 1741 LDKNDSILAPAVFAASNSFPVSVQVNSAGOREEYLLCFHEGFVDFVDSGRSRDLDK 1800
 Db 1741 LDKNDSILAPAVFAASNSFPVSVQVNSAGOREEYLLCFHEGFVDFVDSGRSRDLDK 1800
 Qy 1801 WSRPLAFAYREBYLFTVHNSLEVIEIQARSSAGTPARAYLDIPNRYLGAIPASSGAY 1860
 Db 1801 WSRPLAFAYREBYLFTVHNSLEVIEIQARSSAGTPARAYLDIPNRYLGAIPASSGAY 1860
 Qy 1861 LMSYDDKLAVTCCKGNLVESGTEHHRGPTSRSSPNKRGPTVMEHTKRVASGAPP 1920
 Db 1861 LMSYDDKLAVTCCKGNLVESGTEHHRGPTSRSSPNKRGPTVMEHTKRVASGAPP 1920
 Qy 1921 EGSHPREBPTPHRYEGRTELRDKSPGRPLREKSPGMLSTRRERSGRLFEBOSSRG 1980
 Db 1921 EGSHPREBPTPHRYEGRTELRDKSPGRPLREKSPGMLSTRRERSGRLFEBOSSRG 1980
 Qy 1981 RLPAGAVRTPLSQVNGRGOSASQVFTVNTVYTDNMKCLDNLPAWMSVLRITIQANGEIR 2040
 Db 1981 RLPAGAVRTPLSQVNGRGOSASQVFTVNTVYTDNMKCLDNLPAWMSVLRITIQANGEIR 2040
 Qy 2041 QOVEKSVLRTDYC 2053
 Db 2041 QOVEKSVLRTDYC 2053
 RESULT 4
 US-10-015-011-21
 ; Sequence 21, Application US/10415011
 ; Publication No. US20040053394A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE CORPORATION
 ; APPLICANT: GURURAJAN, Rajagopal
 ; APPLICANT: BAUGHN, Mariah R.
 ; APPLICANT: CHAMLA, Narinder K.
 ; APPLICANT: ELLIOTT, Vicki S.
 ; APPLICANT: XU, Yuming
 ; APPLICANT: ARVIZU, Chandra S.
 ; APPLICANT: VAO, Montique G.
 ; APPLICANT: RAMKOMAR, Jayalakmi
 ; APPLICANT: DING, Li
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: HAFALIA, April J.A.
 ; APPLICANT: NGUYEN, Daniel B.

; APPLICANT: GANDHI, Ameena R.
 ; APPLICANT: LU, Yan
 ; APPLICANT: YUE, Henry
 ; APPLICANT: BURFORD, Neil
 ; APPLICANT: BANDMAN, Olga
 ; APPLICANT: TRIBOULEY, Catherine M.
 ; APPLICANT: LAL, Preeti G.
 ; APPLICANT: RECIPON, Shirley A.
 ; APPLICANT: LU, Dyrung Aina M.
 ; APPLICANT: BOROMSKI, Mark L.
 ; APPLICANT: THORNTON, Michael B.
 ; APPLICANT: SWARNAKER, Anita
 ; APPLICANT: THANGAVELU, Kavitha
 ; APPLICANT: KHAN, Farrah A.
 ; APPLICANT: ISON, Craig H.
 ; TITLE OF INVENTION: HUMAN KINASES
 ; FILE REFERENCE: PI-0262 USN
 ; CURRENT APPLICATION NUMBER: US/10/415,011
 ; PRIOR FILING DATE: 2003-04-18
 ; PRIOR APPLICATION NUMBER: PCT/US01/47728
 ; PRIOR FILING DATE: 2001-10-20
 ; PRIOR APPLICATION NUMBER: US 60/242,410
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: US 60/244,068
 ; PRIOR FILING DATE: 2000-10-27
 ; PRIOR APPLICATION NUMBER: US 60/245,708
 ; PRIOR FILING DATE: 2000-11-03
 ; PRIOR APPLICATION NUMBER: US 60/247,672
 ; PRIOR FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: US 60/249,565
 ; PRIOR FILING DATE: 2000-11-16
 ; PRIOR APPLICATION NUMBER: US 60/252,730
 ; PRIOR FILING DATE: 2000-11-22
 ; PRIOR APPLICATION NUMBER: US 60/250,807
 ; PRIOR FILING DATE: 2000-12-01
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 21
 ; LENGTH: 2054
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20040053394A1 7484498CD1
 US-10-015-011-21
 Query Match 95.6%; Score 10032.5; DB 15; Length 2054;
 Best Local Similarity 95.8%; Pred. No. 0;
 Matches 1981; Conservative 2; Mismatches 4; Indels 81; Gaps 3;
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 Db 1 MLKFKYGANPLDAGAAEPDIASRASHNLFPQKPEPMTQOQWSPLSREGIIDLALFVLE 60
 Qy 61 ECSOPALMKIKVNSVNRKYSDDTIAELOLSAODFEVRSIVGCGHFEVQVVRKANG 120
 Db 61 ECSOPALMKIKVNSVNRKYSDDTIAELOLSAODFEVRSIVGCGHFEVQVVRKANG 120
 Qy 121 DIYAMKVMKKKALLAQEQVSPFEERNNILSRSTSPWIPOLQYAFODKXNLVYLMEEYQPG 180
 Db 121 DIYAMKVMKKKALLAQEQVSPFEERNNILSRSTSPWIPOLQYAFODKXNLVYLMEEYQPG 180
 Qy 181 DLISLNRVEDQDENLQFYLAELILAVSHVLMGYVARDIKPENILVDRGTGHIKLVDP 240
 Db 181 DLISLNRVEDQDENLQFYLAELILAVSHVLMGYVARDIKPENILVDRGTGHIKLVDP 240
 Qy 241 GSAAKKNSNMKNNAKLPICGTPDYMAPEVLTWNNGDGKGYGIDCDMWASGVAYAYEMTYGR 300
 Db 241 GSAAKKNSNMKNNAKLPICGTPDYMAPEVLTWNNGDGKGYGIDCDMWASGVAYAYEMTYGR 300
 Qy 301 SPFAEGTSARTFNINNFQRLKFPDDPKVSSDFDLILQSLCQGERLKFGGLCCHPFF 360
 Db 301 SPFAEGTSARTFNINNFQRLKFPDDPKVSSDFDLILQSLCQGERLKFGGLCCHPFF 360

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QY 361 SKIDMNNIRNSPPFPVTLKSDDOTSNPDEPKNSWSSPCOLSPSGCEELPVGVS 420
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QY 421 YSKALGILGRSESVGLDSPATSSMEKKLLIKSELQDSQDKHMEQENTLRRYS 480
Db 421 YSKALGILGRSESVGLDSPATSSMEKKLLIKSELQDSQDKHMEQENTLRRYS 480
QY 481 EYEAVALSOKVEIKASETQBSLLEODLATYITTCSSLKSLSEQARMEVGOEDDKALQLH 540
Db 481 EYEAVALSOKVEIKASETQBSLLEODLATYITTCSSLKSLSEQARMEVGOEDDKALQLH 540
QY 541 DIREQSRKLOEIKEOGYQAVEEMRLMMNLJEDLVASARRSDLYSESLRESRLAEERK 600
Db 541 DIREQSRKLOEIKEOGYQAVEEMRLMMNLJEDLVASARRSDLYSESLRESRLAEERK 600
QY 541 DIREQSRKLOEIKEOGYQAVEEMRLMMNLJEDLVASARRSDLYSESLRESRLAEERK 600
Db 541 DIREQSRKLOEIKEOGYQAVEEMRLMMNLJEDLVASARRSDLYSESLRESRLAEERK 600
QY 601 RKAATECOHLLAKADQKPEVGEYAKLEKINAEQOKIOLOEKLEKA----- 648
Db 601 RKAATECOHLLAKADQKPEVGEYAKLEKINAEQOKIOLOEKLEKA----- 648
QY 649 ----AKERARELEKLONRDESEGI RKKLVAEERHSL ENKVKLETMERENRLKOD 704
Db 649 ----AKERARELEKLONRDESEGI RKKLVAEERHSL ENKVKLETMERENRLKOD 704
QY 661 NTRQAKERARELEKLONRDESEGI RKKLVAEERHSL ENKVKLETMERENRLKOD 720
Db 661 NTRQAKERARELEKLONRDESEGI RKKLVAEERHSL ENKVKLETMERENRLKOD 720
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Db 705 IOTKSQOIQOMADKILELEEKREAOVSAQHL EYHLKOEKOEYEEKITVLDNOIKKDLAD 764
QY 721 IOTKSQOIQOMADKILELEEKREAOVSAQHL EYHLKOEKOEYEEKITVLDNOIKKDLAD 780
Db 721 IOTKSQOIQOMADKILELEEKREAOVSAQHL EYHLKOEKOEYEEKITVLDNOIKKDLAD 780
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Db 765 KETLENMQRHEEBAHEKGIILSEQAMINAMDSKIRSLBORIVELSEANKLAANSLEPT 824
QY 781 KETLENMQRHEEBAHEKGIILSEQAMINAMDSKIRSLBORIVELSEANKLAANSLEPT 840
Db 781 KETLENMQRHEEBAHEKGIILSEQAMINAMDSKIRSLBORIVELSEANKLAANSLEPT 840
QY 825 QSNMKAQOEIMISELOQKFEYLETOAGKLEAONRKLEBOLEKISHODHSXKRLILEFTL 884
Db 825 QSNMKAQOEIMISELOQKFEYLETOAGKLEAONRKLEBOLEKISHODHSXKRLILEFTL 884
QY 841 QSNMKAQOEIMISELOQKFEYLETOAGKLEAONRKLEBOLEKISHODHSXKRLILEFTL 900
Db 841 QSNMKAQOEIMISELOQKFEYLETOAGKLEAONRKLEBOLEKISHODHSXKRLILEFTL 900
QY 865 REVSLHEHEQKLEKRLQLELOLSIQERESQUTALQAARALESQLRQKLEETTAA 944
Db 865 REVSLHEHEQKLEKRLQLELOLSIQERESQUTALQAARALESQLRQKLEETTAA 944
QY 901 REVSLHEHEQKLEKRLQLELOLSIQERESQUTALQAARALESQLRQKLEETTAA 960
Db 901 REVSLHEHEQKLEKRLQLELOLSIQERESQUTALQAARALESQLRQKLEETTAA 960
QY 945 BEEIOALTNRHDEIQKRPALANSCTVITDLEEQNLUTEDNAELNNQFVLSKQDSEAS 1004
Db 945 BEEIOALTNRHDEIQKRPALANSCTVITDLEEQNLUTEDNAELNNQFVLSKQDSEAS 1004
QY 961 BEEIOALTNRHDEIQKRPALANSCTVITDLEEQNLUTEDNAELNNQFVLSKQDSEAS 1020
Db 961 BEEIOALTNRHDEIQKRPALANSCTVITDLEEQNLUTEDNAELNNQFVLSKQDSEAS 1020
QY 1005 GANDEIYOLRSVVDHARREITEREMOLTSOKOTMALKTTCMLBEOVMDLEALDELLE 1064
Db 1005 GANDEIYOLRSVVDHARREITEREMOLTSOKOTMALKTTCMLBEOVMDLEALDELLE 1064
QY 1021 GANDEIYOLRSVVDHARREITEREMOLTSOKOTMALKTTCMLBEOVMDLEALDELLE 1080
Db 1021 GANDEIYOLRSVVDHARREITEREMOLTSOKOTMALKTTCMLBEOVMDLEALDELLE 1080
QY 1065 KERQMEAWRSVLDGDKSQFECRVRELQOMLDTKOSRARADQRTESQOVVELAVKEHKA 1124
Db 1065 KERQMEAWRSVLDGDKSQFECRVRELQOMLDTKOSRARADQRTESQOVVELAVKEHKA 1124
QY 1081 KERQMEAWRSVLDGDKSQFECRVRELQOMLDTKOSRARADQRTESQOVVELAVKEHKA 1140
Db 1081 KERQMEAWRSVLDGDKSQFECRVRELQOMLDTKOSRARADQRTESQOVVELAVKEHKA 1140
QY 1125 ELIALQOALKKQKLAESLSDYKLANDLEKKHAMELNANASLQOKLETETELKQRLLEQAK 1184
Db 1125 ELIALQOALKKQKLAESLSDYKLANDLEKKHAMELNANASLQOKLETETELKQRLLEQAK 1184
QY 1141 ELIALQOALKKQKLAESLSDYKLANDLEKKHAMELNANASLQOKLETETELKQRLLEQAK 1200
Db 1141 ELIALQOALKKQKLAESLSDYKLANDLEKKHAMELNANASLQOKLETETELKQRLLEQAK 1200
QY 1185 LOQQMDLOKNHIFRLTOGLOEALDRADLLKTERSDLEKTOLENTIOVLYSHEKVKMGSTISQ 1244
Db 1185 LOQQMDLOKNHIFRLTOGLOEALDRADLLKTERSDLEKTOLENTIOVLYSHEKVKMGSTISQ 1244
QY 1201 LOQQMDLOKNHIFRLTOGLOEALDRADLLKTERSDLEKTOLENTIOVLYSHEKVKMGSTISQ 1260
Db 1201 LOQQMDLOKNHIFRLTOGLOEALDRADLLKTERSDLEKTOLENTIOVLYSHEKVKMGSTISQ 1260
QY 1245 QTKLIDFLQANWDQPAKKKKGLFSRRKEDPALPTQVPLQYNELKLALKEKARCALESEA 1304
Db 1245 QTKLIDFLQANWDQPAKKKKGLFSRRKEDPALPTQVPLQYNELKLALKEKARCALESEA 1304
QY 1261 QTKLIDFLQANWDQPAKKKKGLFSRRKEDPALPTQVPLQYNELKLALKEKARCALESEA 1305
Db 1261 QTKLIDFLQANWDQPAKKKKGLFSRRKEDPALPTQVPLQYNELKLALKEKARCALESEA 1305
QY 1305 LOKTRIEARSAREEAHAKADHDPSTPATARQOIASAIYRSPEHOPSAWSLAPSS 1364
Db 1305 LOKTRIEARSAREEAHAKADHDPSTPATARQOIASAIYRSPEHOPSAWSLAPSS 1364
QY 1306 LOKTRIEARSAREEAHAKADHDPSTPATARQOIASAIYRSPEHOPSAWSLAPSS 1365
Db 1306 LOKTRIEARSAREEAHAKADHDPSTPATARQOIASAIYRSPEHOPSAWSLAPSS 1365
QY 1365 RRKESSTPEEFSRRLKERGMHNIIPHRFNVGLNMRATKAVCLDPTHFERQASKLECOVM 1424
Db 1365 RRKESSTPEEFSRRLKERGMHNIIPHRFNVGLNMRATKAVCLDPTHFERQASKLECOVM 1424
QY 1366 RRKESSTPEEFSRRLKERGMHNIIPHRFNVGLNMRATKAVCLDPTHFERQASKLECOVM 1425
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QY 1425 CHPKSTCLPATCGIPAEYATHFTEAFCDKKNNSGLOQTKERSSSLHEGMKVPRNKR 1484
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QY 1485 GQGGMDRKTYVLESGKVL IYDNEAREAGORPVSEFELCLPDQDVSIHGAVGASELANAK 1544
Db 1485 GQGGMDRKTYVLESGKVL IYDNEAREAGORPVSEFELCLPDQDVSIHGAVGASELANAK 1545
QY 1545 A-----EKADAKL 1554
Db 1545 ADVPYILKMHSHPTTWCGRFTLYLLAPSFDKQRMWTALESVAGVRSEKADAKL 1605
QY 1555 IGSNLKLEGGDRLLMNCCTLPSPDOVLTGREGIYALNLTKNLTHTPRTGAVQIYI 1614
Db 1555 IGSNLKLEGGDRLLMNCCTLPSPDOVLTGREGIYALNLTKNLTHTPRTGAVQIYI 1614
QY 1606 IGSNLKLEGGDRLLMNCCTLPSPDOVLTGREGIYALNLTKNLTHTPRTGAVQIYI 1665
Db 1606 IGSNLKLEGGDRLLMNCCTLPSPDOVLTGREGIYALNLTKNLTHTPRTGAVQIYI 1665
QY 1615 KDLKELMIAGEERALCLVDYKVKVQSLAQSHLPAPQDISPNIPEAVGCHLFGAKIEN 1674
Db 1615 KDLKELMIAGEERALCLVDYKVKVQSLAQSHLPAPQDISPNIPEAVGCHLFGAKIEN 1675
QY 1666 KDLKELMIAGEERALCLVDYKVKVQSLAQSHLPAPQDISPNIPEAVGCHLFGAKIEN 1725
Db 1666 KDLKELMIAGEERALCLVDYKVKVQSLAQSHLPAPQDISPNIPEAVGCHLFGAKIEN 1725
QY 1675 GLCTCAMPSPKVILIRNENISKYICIRKEIETSEPCSIHFTNYSILIGTNKFEYIDMKO 1734
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QY 1726 GLCTCAMPSPKVILIRNENISKYICIRKEIETSEPCSIHFTNYSILIGTNKFEYIDMKO 1785
Db 1726 GLCTCAMPSPKVILIRNENISKYICIRKEIETSEPCSIHFTNYSILIGTNKFEYIDMKO 1785
QY 1735 YLSEFELDKNDHSLAPAFVASSNSFPVSIYOUNSAGOREYLLCFHERGFVDSYGRS 1794
Db 1735 YLSEFELDKNDHSLAPAFVASSNSFPVSIYOUNSAGOREYLLCFHERGFVDSYGRS 1845
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Db 1795 RTDILKMSRLPLAFYREPLYFTVHFNSLEVIETIQARSAGTPARAYLIDINPRILGPAI 1905
QY 1846 RTDILKMSRLPLAFYREPLYFTVHFNSLEVIETIQARSAGTPARAYLIDINPRILGPAI 1905
Db 1846 RTDILKMSRLPLAFYREPLYFTVHFNSLEVIETIQARSAGTPARAYLIDINPRILGPAI 1905
QY 1855 SSGAIIYLAASYODKLRVYCCGKGLVKBSGTEHHRGPSTSRSPNKGPPYNEHITKRYA 1914
Db 1855 SSGAIIYLAASYODKLRVYCCGKGLVKBSGTEHHRGPSTSRSPNKGPPYNEHITKRYA 1965
QY 1906 SSGAIIYLAASYODKLRVYCCGKGLVKBSGTEHHRGPSTSRSPNKGPPYNEHITKRYA 1965
Db 1906 SSGAIIYLAASYODKLRVYCCGKGLVKBSGTEHHRGPSTSRSPNKGPPYNEHITKRYA 1965
QY 1915 SSPAPBEGSPHREPSPTPHRREGRTLEBRDKSPGRPLERKSPGRLSTREBSPGLF 1974
Db 1915 SSPAPBEGSPHREPSPTPHRREGRTLEBRDKSPGRPLERKSPGRLSTREBSPGLF 1974
QY 1966 SSPAPBEGSPHREPSPTPHRREGRTLEBRDKSPGRPLERKSPGRLSTREBSPGLF 2025
Db 1966 SSPAPBEGSPHREPSPTPHRREGRTLEBRDKSPGRPLERKSPGRLSTREBSPGLF 2025
QY 1975 EDSRGRLLPAGAVRTPLSQVKKRGQSA 2002
Db 1975 EDSRGRLLPAGAVRTPLSQVKKRGQSA 2002
QY 2026 EDSRGRLLPAGAVRTPLSQVKKRGQSA 2053
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RESULT 5
 US-10-028-946-2
 ; Sequence 2, Application US/10028946
 ; Publication No. US20020123622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YU, Xuanchuan
 ; APPLICANT: Miranda, Maricar
 ; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
 ; FILE REFERENCE: LEX-0289-USA
 ; CURRENT APPLICATION NUMBER: US/10/028,946
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: US 60/258,335
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 2054
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-028-946-2

Query Match 95.5%; Score 10022.5; DB 13; Length 2054;
 Best Local Similarity 95.7%; Pred. No. 0;
 Matches 1979; Conservative 3; Mismatches 5; Indels 81; Gaps 3;

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 Db 241 GSAAKNSKMNNAKPIGTPDYMAPEVLTVMNGDGKTYGLDCDMMWSGVIAEM1YGR 300
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 Db 361 SKIDMNNINNSPPFPVPTLKSDDDTSNPDPEKNSWVSSPCQLSPSGSGEELPFVGS 420
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 Db 541 DI1REGSRKLOEIKEGEYQAOVEEMRLMMQLEEDIVSARRSDLYSELSRESRLAEBRK 600
 Qy 601 RKATTEGONHLAKQOGKPEVGYATLKEKINAEQOLKIOELQKLEKA----- 648
 Db 601 RKATTEGONHLAKQOGKPEVGYATLKEKINAEQOLKIOELQKLEKA----- 648
 Qy 649 ----AKERARELEKJONREDSSEGIKXKLVEAEERHSLNNVKKLETMERENKLLKOD 704
 Db 649 ----AKERARELEKJONREDSSEGIKXKLVEAEERHSLNNVKKLETMERENKLLKOD 704
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 Db 705 IOTKSQOIQOMADKILEBEKREAOVSAQHLEVHLKQKQHYBEKIKVLDNQIKKDLAD 764
 Qy 765 KETLEMMQORHEBEAHEKGIISBOQAMINANDSKIRSLBORIVELSEANKLAANSLSLT 824
 Db 765 KETLEMMQORHEBEAHEKGIISBOQAMINANDSKIRSLBORIVELSEANKLAANSLSLT 824
 Qy 825 OBNMKAQOEMISBLRQOKFYLETQAGKLEAONRKLEBOLEKISHOHSNDKNRLLLEETFL 884
 Db 825 OBNMKAQOEMISBLRQOKFYLETQAGKLEAONRKLEBOLEKISHOHSNDKNRLLLEETFL 884
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 Db 885 REVSLEHEBOKLEKQKTELQSLQOERESQUTALQANARAALESQURQAKTELEETTA 944
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 Db 945 BEBIOALTNHDEIOKFPALANSCTVITDLSEQLNQLTEDNAELANNQNFYLSKQJDEAS 1004
 Qy 1005 GANDEIVQARSEVDHNRRTITEREMQJTSOKOTMEALKTTCMLLEBQWDLBALNDELLE 1064
 Db 1005 GANDEIVQARSEVDHNRRTITEREMQJTSOKOTMEALKTTCMLLEBQWDLBALNDELLE 1064
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Qy 1125 ETLALQALKEOKLKAESLSDKLNDLEKKAMLEMMARSLQOKLETTERELKORILEBOAK 1184
 Db 1141 ETLALQALKEOKLKAESLSDKLNDLEKKAMLEMMARSLQOKLETTERELKORILEBOAK 1200
 Qy 1185 LQOQNDLOKNNHIFRLTQOGLQALDRADLLKTERSDLEYOLENIQVLYSHEKVMESTISO 1244
 Db 1201 LQOQNDLOKNNHIFRLTQOGLQALDRADLLKTERSDLEYOLENIQVLYSHEKVMESTISO 1260
 Qy 1245 QTKLIDFLQAKNDOPAKKKKGLFSRRKEDPALPTQVPLQYNELKALBEKAKCALEBEA 1304
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 Db 1306 LQKTRIELSAREBAHRAKATDHPHSTPATARQOJAMSATVRSPEHOSAMSILAPSS 1365
 Qy 1365 RRKESSTPEESRRRLKERMHNNIPIHFNVLNMRATKCAVCLDTYHFGQASKECQVM 1424
 Db 1366 RRKESSTPEESRRRLKERMHNNIPIHFNVLNMRATKCAVCLDTYHFGQASKECQVM 1425
 Qy 1425 CHPKSSTCLPATCGLPABEYATHTFAFCRDKNNSPGLQTKESPSSILHEGMMKVPRNNR 1484
 Db 1426 CHPKSSTCLPATCGLPABEYATHTFAFCRDKNNSPGLQTKESPSSILHEGMMKVPRNNR 1485
 Qy 1485 GQOQNDKRYIVLEGSVULYDNEAREAGORPYEPEBELCLPDGDVSTHGAVGASELANATK 1544
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 Qy 1545 A-----EKAEDAKL 1554
 Db 1546 ADVPIYKRNESHPRHTTCWGRTLYLAPSPFPRKQWMTLSEVNAVAGRVREKAEADAL 1605
 Qy 1555 LQNSLLKLEGGDRDLDMNCTLPSPDOVVLVGTSEGLYALNVLKNSLTHVPGICAVFOIYI 1614
 Db 1606 LQNSLLKLEGGDRDLDMNCTLPSPDOVVLVGTSEGLYALNVLKNSLTHVPGICAVFOIYI 1665
 Qy 1615 KOLEKLMJAGEBRALCLVDYKXVQVQSLAQSHLPAPQDIPSPNIFEAIVKCHLFGAKIEN 1674
 Db 1666 KOLEKLMJAGEBRALCLVDYKXVQVQSLAQSHLPAPQDIPSPNIFEAIVKCHLFGAKIEN 1725
 Qy 1675 GLCICAMPKSVIIRYENLSKYCIKREIETSEPCSCIHFNYSILGTNKFEIEMQK 1734
 Db 1726 GLCICAMPKSVIIRYENLSKYCIKREIETSEPCSCIHFNYSILGTNKFEIEMQK 1785
 Qy 1735 YTLBEFLDKNDHSLAPVAFPAASNSFPVSIQVNSAGOREEYLLCFHEGVFVDSYGRS 1794
 Db 1786 YTLBEFLDKNDHSLAPVAFPAASNSFPVSIQVNSAGOREEYLLCFHEGVFVDSYGRS 1845
 Qy 1795 RTDIDLKMSRLPLAFAYREBYLFTVTHNSLEVEIOPARSSAGTPARAYLDIPNRYLGPXI 1854
 Db 1846 RTDIDLKMSRLPLAFAYREBYLFTVTHNSLEVEIOPARSSAGTPARAYLDIPNRYLGPXI 1905
 Qy 1855 SSGAIYILASSYODKLRVICCKGNLVESGTEHHRGPTSRSSPNKRGPTTYNHEHTKXA 1914
 Db 1906 SSGAIYILASSYODKLRVICCKGNLVESGTEHHRGPTSRSSPNKRGPTTYNHEHTKXA 1965
 Qy 1945 SSPAPPEGSHPRESTPHRYAGRTELRDKSPGRPLEREXSPGRMLSTRERSPGRL 1974
 Db 1966 SSPAPPEGSHPRESTPHRYAGRTELRDKSPGRPLEREXSPGRMLSTRERSPGRL 2025
 Qy 1975 EDSRGRPLPAGAVRTPLSQVKKRGQSA 2002
 Db 2026 EDSRGRPLPAGAVRTPLSQVKKRGQSA 2053

RESULT 6

US-10-618-941-67
 ; Sequence 67, Application US/10618941
 ; Publication No. US2004019792A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WHYTE, DAVID
 ; APPLICANT: MANNING, GERARD

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; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 67
; LENGTH: 2055
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-618-941-67

Query Match      95.4%; Score 10011; DB 16; Length 2055;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1979; Conservative 3; Mismatches 5; Indels 82; Gaps 4;

QY      1 MLKFKTGANNPLDAGAAEPILASASRLNLPFGCKPFPMTQQOMSPLSREGTLDALFVLFE 60
DB      1 MLKFKTGANNPLDAGAAEPILASASRLNLPFGCKPFPMTQQOMSPLSREGTLDALFVLFE 60
QY      61 ECGSOPALMKIKHVSNFVRK-YSDPTIAELOPSAKDFEVSIVGCGHFAEYQVVAEKAT 119
DB      61 ECGSOPALMKIKHVSNFVPEVYSDPTIAELOPSAKDFEVSIVGCGHFAEYQVVAEKAT 120
QY      120 GDIYANKVKKKALLAQEOVSFPEEERNILSRSTSPWITPOLQYAFODKNHLYIMEEYQNG 179
DB      121 GDIYANKVKKKALLAQEOVSFPEEERNILSRSTSPWITPOLQYAFODKNHLYIMEEYQNG 180
QY      180 GDILSLINVEODLDNLIQFYLAELILAVHSVHMGVYHDKPENIILVDRIGHIKLYND 239
DB      181 GDILSLINREBDLDNLIQFYLAELILAVHSVHMGVYHDKPENIILVDRIGHIKLYND 240
QY      240 FGSAAKONSNNKVNNAKLPIGTDPYMAPEVLTVMNGDGKGYGLDCDMSVGVIAEMIVG 299
DB      241 FGSAAKONSNNKVNNAKLPIGTDPYMAPEVLTVMNGDGKGYGLDCDMSVGVIAEMIVG 300
QY      300 RSPFPAAGTSARTNNIMNFORPLKFPDDPKVSSDFDLIQSLICGQEKRLKFPGLCCHFP 359
DB      301 RSPFPAAGTSARTNNIMNFORPLKFPDDPKVSSDFDLIQSLICGQEKRLKFPGLCCHFP 360
QY      360 FSKIDNNNTINSPRPVPTKSDPDTSNPDEPEKNSSWSSPCQLSPSGSGEELFPVGF 419
DB      361 FSKIDNNNTINSPRPVPTKSDPDTSNPDEPEKNSSWSSPCQLSPSGSGEELFPVGF 420
QY      420 SYSKALGILGRSESVSGLDSPAKTSSMEKKLIIKSKELQDSQDKCHKMEOEWTRLHRRV 479
DB      421 SYSKALGILGRSESVSGLDSPAKTSSMEKKLIIKSKELQDSQDKCHKMEOEWTRLHRRV 480
QY      480 SEVEAVLSQKEVELKASETORSLIEDPLATYITEGSLKRSLEQAAWMSVQEDDKALQLL 539
DB      481 SEVEAVLSQKEVELKASETORSLIEDPLATYITEGSLKRSLEQAAWMSVQEDDKALQLL 540
QY      540 HDIREOSRKLOEIKEOGYAQVEMRLMNQOLEEDIVSARRSDLYESELSRESLAAEEF 599
DB      541 HDIREOSRKLOEIKEOGYAQVEMRLMNQOLEEDIVSARRSDLYESELSRESLAAEEF 600
QY      600 KRKATECOHKLAKADQKPEVEAYAKLEKINAEOQLIQELOEKLKA----- 648
DB      601 KRKATECOHKLAKADQKPEVEAYAKLEKINAEOQLIQELOEKLKA----- 660
QY      649 -----AKERAPRELKQNRNEDSEGRKQVLAEEERHSLKQVLEMERREARLKD 703
DB      661 QNIRQAERERARELEKQNRNEDSEGRKQVLAEEERHSLKQVLEMERREARLKD 720
QY      704 DIQTSQOIQOMADKILELEKEKREAVQASHLEVLHKQEQHYEEKIKVLDNQIKKDLA 763
DB      721 DIQTSQOIQOMADKILELEKEKREAVQASHLEVLHKQEQHYEEKIKVLDNQIKKDLA 780
QY      764 DKETLENNQPHHEEAHEKGIILSEQKAMINAMDSKIRSLERQIVLESEANKLANSSLF 823
DB      764 DKETLENNQPHHEEAHEKGIILSEQKAMINAMDSKIRSLERQIVLESEANKLANSSLF 823
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DB      781 DKETLENNQPHHEEAHEKGIILSEQKAMINAMDSKIRSLERQIVLESEANKLANSSLF 840
QY      824 TORNNKAOEEMISLIRQOKFLYLETQAGKLEPQNRKLEBOLEKISHQSHSDKNRLLELETR 883
DB      841 TORNNKAOEEMISLIRQOKFLYLETQAGKLEPQNRKLEBOLEKISHQSHSDKNRLLELETR 900
QY      884 LREYSLHEEOKLEKQLETLQSLQERESQTLQAAARALBSQLOAKTELEETTAEE 943
DB      901 LREYSLHEEOKLEKQLETLQSLQERESQTLQAAARALBSQLOAKTELEETTAEE 960
QY      944 ABEELIOLTARDEIQRKFDALRNSCTVIYTDLEBQNLQTEDNABLNQNFYLSKOLDEA 1003
DB      961 ABEELIOLTARDEIQRKFDALRNSCTVIYTDLEBQNLQTEDNABLNQNFYLSKOLDEA 1020
QY      1004 SGANDEIYQALSEVDHLRREITTEEMOULTSQOMELAKTCTMLEBQVMDLEALNBEIL 1063
DB      1021 SGANDEIYQALSEVDHLRREITTEEMOULTSQOMELAKTCTMLEBQVMDLEALNBEIL 1080
QY      1064 EKERQWEMARSVLGDEKSQFECRVARELQRMIDTEKQSRARADORTTESRQVVELAVKXK 1123
DB      1081 EKERQWEMARSVLGDEKSQFECRVARELQRMIDTEKQSRARADORTTESRQVVELAVKXK 1140
QY      1124 AEIILAQALKBQKIKAESISDKLNDLEKKGAMIBNARSLQOKLETRELEKORLLEBQA 1183
DB      1141 AEIILAQALKBQKIKAESISDKLNDLEKKGAMIBNARSLQOKLETRELEKORLLEBQA 1200
QY      1184 KLQOQMDLQKXNHIFPLTQGLQALDRADLTLTERSDELYOLENIQVLYSHEKVMKEGTS 1243
DB      1201 KLQOQMDLQKXNHIFPLTQGLQALDRADLTLTERSDELYOLENIQVLYSHEKVMKEGTS 1260
QY      1244 QOTKLIDFLQAKMDQPAKKKKGLPSRRKEDPALPTQVLEQVNELEKALEKEXKARCALEEE 1303
DB      1261 QOTKLIDFLQAKMDQPAKKKK-----VLEQVNELEKALEKEXKARCALEEE 1305
QY      1304 ALQKTRIELRSAREEAARKATDHPHNESTPATTAQOIMSAIVSPHEQPSAMSLAPPS 1363
DB      1306 ALQKTRIELRSAREEAARKATDHPHNESTPATTAQOIMSAIVSPHEQPSAMSLAPPS 1365
QY      1364 SRRKESSTPEEPSRRLKERMHNIIPHRPNVGLNBRATCAVCLDTHVHGROASKLCEQV 1423
DB      1366 SRRKESSTPEEPSRRLKERMHNIIPHRPNVGLNBRATCAVCLDTHVHGROASKLCEQV 1425
QY      1424 MCHPRCSTCLPATCGLPAEYATHFTFATCRDQMSPGIQTKEPSSSLHLEGMKYPRNNK 1483
DB      1426 MCHPRCSTCLPATCGLPAEYATHFTFATCRDQMSPGIQTKEPSSSLHLEGMKYPRNNK 1485
QY      1484 RQOQGMDRKTYVLBESKTYLYDNEAREAGQRPVEFEELCLPDGIVSIHGAVGASRLATA 1543
DB      1486 RQOQGMDRKTYVLBESKTYLYDNEAREAGQRPVEFEELCLPDGIVSIHGAVGASRLATA 1545
QY      1544 KA-----EKAADAK 1553
DB      1546 KADVAYILKMHSHPTTCMPGRTLYLLAPSPFDKQRMWTALLESVYVAGRVSEKABADAK 1605
QY      1554 ILGNSILKLEGGDRLDNMCCTLPSPQVVLVGTBEGYALANTVKNLTHVPGIGAVFOIYI 1613
DB      1606 ILGNSILKLEGGDRLDNMCCTLPSPQVVLVGTBEGYALANTVKNLTHVPGIGAVFOIYI 1665
QY      1614 IYDLKELMLIAEERBALCLVDYKXKOSLAOSHLPQAPDISPNIPEAVNGKLPFAGKLE 1673
DB      1666 IYDLKELMLIAEERBALCLVDYKXKOSLAOSHLPQAPDISPNIPEAVNGKLPFAGKLE 1725
QY      1674 NGLCICAMPSPKVILIRVYENLSKYCIKRELETSPSCGCIHFTNYSILIGTKFYEIDMK 1733
DB      1726 NGLCICAMPSPKVILIRVYENLSKYCIKRELETSPSCGCIHFTNYSILIGTKFYEIDMK 1785
QY      1734 QYTLLEFDLXNDHSLAPAVFAASSNPYSIYQVNSAGOREYILLCFHFRGIFUNSYGR 1793
DB      1786 QYTLLEFDLXNDHSLAPAVFAASSNPYSIYQVNSAGOREYILLCFHFRGIFUNSYGR 1845
QY      1794 SRTDILKMSRLPLAFYREPYLFVTHFNSLEVIEIQASSSACTPARAYLDIPNPRYLGA 1853
DB      1846 SRTDILKMSRLPLAFYREPYLFVTHFNSLEVIEIQASSSACTPARAYLDIPNPRYLGA 1905
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QY 1854 ISSGAIIYLASSYODKLRVYCCGNLYKESGTEHHRGPTSRSSPNKRGPTVNEHTKRV 1913
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DB 1906 ISSGAIIYLASSYODKLRVYCCGNLYKESGTEHHRGPTSRSSPNKRGPTVNEHTKRV 1965
| | | | |
QY 1914 ASSPAPEGSPHREPRESTPHRREGRTELRBDKSPGRPLEREXSPGRMLSTRERSPGR 1973
| | | | |
DB 1966 ASSPAPEGSPHREPRESTPHRREGRTELRBDKSPGRPLEREXSPGRMLSTRERSPGR 2025
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QY 1974 FEDSSRGRLPAGAVRTPLSQVNKGRGQSA 2002
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DB 2026 FEDSSRGRLPAGAVRTPLSQVNKVMPOSS 2054
| | | | |
RESULT 7
US-09-964-956-9
; Sequence 9, Application US/09964956
; Publication No. US20040043926A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Elberman, Karen
; APPLICANT: Grose, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine B
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimets, Richard A
; TITLE OF INVENTION: No. US20040043926A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/09/964, 956
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235, 631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235, 633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235, 808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236, 064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236, 065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236, 066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236, 135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237, 434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238, 321
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238, 399
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238, 396
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/276, 667
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/294, 823
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/304, 868
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 9
; LENGTH: 2066
; TYPE: PRT
; ORGANISM: Homo sapiens

Handwritten: 21402-124
No v 34

US-09-964-956-9
Query Match 95.4%; Score 10007; DB 11; Length 2066;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1979; Conservative 3; Mismatches 7; Indels 82; Gaps 4;
QY 1 MCKFYGANPLDAGAAEPPIASRRLNLFQGGKPPMTQOQMSPLSRGIIIDALFVLE 60
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DB 61 ECGOPALMKIKHVSFNVRKYSDTIAELOPSADFEVRSIVGCGFAVQVVEKATG 120
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QY 121 DIYAKVMKKALLAOEYVSPFEERNTLSNSTSWIPOLQYAFODKXNLYMEYOPG 180
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DB 121 DIYAKVMKKALLAOEYVSPFEERNTLSNSTSWIPOLQYAFODKXNLYMEYOPG 180
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DB 181 DLSLNLNREDOJDNLIQFYLAELILAVSHVHLGVYHRDIKPNILVDRGHTKLYPF 240
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QY 241 GSAATONSXKVNNAKLPITGPDYMAPEVLTWNNGDGKGTGGLDCDMSVGVIAEM1YGR 300
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DB 360 SKIDNNNIRNSPPVPVPTLKSDPDTNFDPEKNSWSSPCQSPSGSGELPVGVS 420
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QY 421 YSKALGIIGRSBSVSGLDSPAKTSMEKULIKSEKLODSQDKHKMEQETRLHRYVS 480
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DB 421 YSKALGIIGRSBSVSGLDSPAKTSMEKULIKSEKLODSQDKHKMEQETRLHRYVS 480
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QY 481 EVEAVLSQKEVELKASETORSLEODLATYITEGSLKRSLEQAMENYQEBDKALQLIH 540
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QY 540 DREOSRKLQETKEOEYQAVQEMRLMNOLEEDIVSARRSDLYESELRESRLAABERK 600
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QY 649 ----AKERAERELEKLNREDSSEGIKKLVABERRHSLNKVRLLETMERRENRLKOD 704
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DB 720 IOTKSQOIQOMADKLTLEBEKGRQAVQAHLEVLKQKQYEEKIKYLNQIKKDLAD 779
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QY 765 KETLENMMQORHEEAEHKGKILSEQKAMINAMDSKIRSLERIVELSEANKLAANSLFT 824
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DB 765 KETLENMMQORHEEAEHKGKILSEQKAMINAMDSKIRSLERIVELSEANKLAANSLFT 824
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DB 825 QNMKAQEBMISLQKQKPYLETQNGKLEAONRKLEBOLKISHODSDKNRLLELETRL 884
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QY 840 QNMKAQEBMISLQKQKPYLETQNGKLEAONRKLEBOLKISHODSDKNRLLELETRL 899
| | | | |
DB 840 QNMKAQEBMISLQKQKPYLETQNGKLEAONRKLEBOLKISHODSDKNRLLELETRL 899
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QY 885 REVLSLEHEQKLEKROLTELQLSQERESQTLQAABALESQLOKAKTELESETTEA 944
| | | | |
DB 885 REVLSLEHEQKLEKROLTELQLSQERESQTLQAABALESQLOKAKTELESETTEA 944
| | | | |
QY 900 REVLSLEHEQKLEKROLTELQLSQERESQTLQAABALESQLOKAKTELESETTEA 959
| | | | |
DB 900 REVLSLEHEQKLEKROLTELQLSQERESQTLQAABALESQLOKAKTELESETTEA 959
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QY 945 EEEIOALTARDEIORKFDALRNSCTVITDLEBQNLQTEBNAELANNQNFYLSKQJDEAS 1004
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DB 945 EEEIOALTARDEIORKFDALRNSCTVITDLEBQNLQTEBNAELANNQNFYLSKQJDEAS 1004
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QY 960 EEEIOALTARDEIORKFDALRNSCTVITDLEBQNLQTEBNAELANNQNFYLSKQJDEAS 1019
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QY 1005 GANDEIYOLASEVDHLRREITEREMOITSQOTMEALKTTCMLBERQVMDLEALINDELLE 1064
DB 1020 GANDEIYOLASEVDHLRREITEREMOITSQOTMEALKTTCMLBERQVMDLEALINDELLE 1079
QY 1065 KERQWEMANSVLGDEKSOFECEVRRELOMDTEKOSRARADORTESROVVELAVEHKA 1124
DB 1080 KERQWEMANSVLGDEKSOFECEVRRELOMDTEKOSRARADORTESROVVELAVEHKA 1139
QY 1125 EIALAOALKEOQLKAEBSLSDKINDLEKXAMLENNARSIQOQLTERELKORLLEBOAK 1184
DB 1140 EIALAOALKEOQLKAEBSLSDKINDLEKXAMLENNARSIQOQLTERELKORLLEBOAK 1199
QY 1185 LOOQMDLOKXHTFRLQOGLQEALDRADILKTESDIEYOLENTQUTYSHKXVMEGTISQ 1244
DB 1200 LOOQMDLOKXHTFRLQOGLQEALDRADILKTESDIEYOLENTQUTYSHKXVMEGTISQ 1259
QY 1245 QTKLIDFLQAKMDQPAKKGGLFSRRKEDPALPTQVPLQYNELKALEKAKCALEBA 1304
DB 1260 QTKLIDFLQAKMDQPAKKGGLFSRRKEDPALPTQVPLQYNELKALEKAKCALEBA 1304
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DB 1305 LOKTRIELASAREBAHRKATDHPHSTPATARQOJAMSATVRSPEHOPSAMSLAPSS 1364
QY 1365 RRKESSTPEEFBRRLKERMHNNIPHRFNGLMMBATKCAVCIDTVHFGROASKLECOYM 1424
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DB 1605 LGNBIKLKIEGDRLLDMNCTLPSSDOVLYGTIEGILYALNVLKNSLTHVPGIAGVQIYI 1664
QY 1615 KOLEKLIMAGEERALCTVDVKVQOSLAOSHLPAOPDISPUIFEAVVGCHLFGAGKLEN 1674
DB 1665 KOLEKLIMAGEERALCTVDVKVQOSLAOSHLPAOPDISPUIFEAVVGCHLFGAGKLEN 1724
QY 1675 GLCTICAMPSSKVILRYNENTLKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKO 1734
DB 1725 GLCTICAMPSSKVILRYNENTLKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKO 1784
QY 1735 YLTFEELDKNHSALPAVFAASSNSFPVSIYQVNSAGOREYLLCTHEFGVCFVDSYGRS 1794
DB 1785 YLTFEELDKNHSALPAVFAASSNSFPVSIYQVNSAGOREYLLCTHEFGVCFVDSYGRS 1844
QY 1795 RTDILKMSRLPLAFAYREPYLFVTHFNSLEVEIEIQAASSAGTPARAYLIDINPRYLGPAT 1854
DB 1845 RTDILKMSRLPLAFAYREPYLFVTHFNSLEVEIEIQAASSAGTPARAYLIDINPRYLGPAT 1904
QY 1855 SSGAIYLLASSYQDKIRVICCKGNLVKESGTEHHRRPSTSRSSPNKRGPPYNEHTTKVA 1914
DB 1905 SSGAIYLLASSYQDKIRVICCKGNLVKESGTEHHRRPSTSRSSPNKRGPPYNEHTTKVA 1964
QY 1915 SSPAPPEGSHPRESTPHRRREGTELRKDKSPERPIERKXSGFKMLSTRRESPGRLF 1974
DB 1965 SSPAPPEGSHPRESTPHRRREGTELRKDKSPERPIERKXSGFKMLSTRRESPGRLF 2024
QY 1975 EDSRGRPLPAGAVRTPLSQVKKGRQASQV 2005
DB 2025 EDSRGRPLPAGAVRTPLSQVKKGRQASQV 2055

RESULT 8
US-10-262-511-14
; Sequence 14, Application US/10262511
; Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patirajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malpankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zernusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Raestelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: Cursaseqdist version 0.1
SEQ ID NO 14
LENGTH: 2066
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-14

Query Match 95.4%; Score 10007; DB 15; Length 2066;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1979; Conservative 3; Mismatches 7; Indels 82; Gaps 4;
QY 1 MLKFYGAARNPLDAGAAEPASRASRLNLFQGGKPPFMTQQQWSPLSRGILDALFVLFE 60

Db 1 MLFFKXGARNPLDAGAAEPJASRASRLNLFQCGKPPFMTQOQMSPLSREGILDALFLVFE 60
 Qy 61 ESOOPAMTKIYHNSVNRKXSDTIAELQELQPSAKDPEVSVJGCGHFAVQVVRKATC 120
 Db 61 ESOOPAMTKIYHNSVNRKXSDTIAELQELQPSAKDPEVSVJGCGHFAVQVVRKATC 120
 Qy 121 DIYAMKVMKKKALLAOEOVSFFEEERNIISRSTSPMIPOLQVAFODKNHLYLMEETOPGG 180
 Db 121 DIYAMKVMKKKALLAOEOVSFFEEERNIISRSTSPMIPOLQVAFODKNHLYLMEETOPGG 180
 Qy 181 DLSLNLRYEDQDENLLOFYLAELLLAVSHVLMGVHRDIXENILVDRTHIKLVDF 240
 Db 181 DLSLNLRYEDQDENLLOFYLAELLLAVSHVLMGVHRDIXENILVDRTHIKLVDF 240
 Qy 241 GSAKKNNSKMNNAKPIGTPDYMAPEVLTVMNGDGKITYGLDCCDMSVGVIAEM1YGR 300
 Db 241 GSAKKNNSKMNNAKPIGTPDYMAPEVLTVMNGDGKITYGLDCCDMSVGVIAEM1YGR 300
 Qy 301 SPPAEGTSARTENNINNFORFLKFPDPPKVSDFLDLQSLGQKERLKFEGLCCHPFF 360
 Db 301 SPPAEGTSARTENNINNFORFLKFPDPPKVSDFLDLQSLGQKERLKFEGLCCHPFF 360
 Qy 361 SKIDMNNIRNSPPFVPTLKSDDTSNFBEPKNSWVSSPCQLSPSGSGEELPFVGS 420
 Db 361 SKIDMNNIRNSPPFVPTLKSDDTSNFBEPKNSWVSSPCQLSPSGSGEELPFVGS 420
 Qy 421 YSKALGILGRSESVGLDSPAATSSMEKKL1KSKBLDSDQKCHMOEOTRLHRRVS 480
 Db 421 YSKALGILGRSESVGLDSPAATSSMEKKL1KSKBLDSDQKCHMOEOTRLHRRVS 480
 Qy 481 EYKAVLSOKEVELKASSETORSLLEODLATYITECSSLKSLEQARHVSQEDKALQOLH 540
 Db 481 EYKAVLSOKEVELKASSETORSLLEODLATYITECSSLKSLEQARHVSQEDKALQOLH 540
 Qy 541 D1REOSRKLQEIKEOBYOAOVEEMRLMNOLEEDLVARSRRSDLYSESLAESRLAEEFK 600
 Db 541 D1REOSRKLQEIKEOBYOAOVEEMRLMNOLEEDLVARSRRSDLYSESLAESRLAEEFK 600
 Qy 540 D1REOSRKLQEIKEOBYOAOVEEMRLMNOLEEDLVARSRRSDLYSESLAESRLAEEFK 599
 Db 540 D1REOSRKLQEIKEOBYOAOVEEMRLMNOLEEDLVARSRRSDLYSESLAESRLAEEFK 599
 Qy 601 RKA7ECOHKLLKXKDGQKPEVGEYAKLEKINAEOQLKIOELOEKLEKA----- 648
 Db 601 RKA7ECOHKLLKXKDGQKPEVGEYAKLEKINAEOQLKIOELOEKLEKA----- 648
 Qy 649 ----AAEBAERLEK1ONREDSSEGT RKTUVEAEBRRHSLENVKRLTETMERENLXKD 704
 Db 649 ----AAEBAERLEK1ONREDSSEGT RKTUVEAEBRRHSLENVKRLTETMERENLXKD 704
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 Db 705 IOTKSQOIQOMADKILEBEKREAOVSAOHLFVHLKOKEOHYEEKIKVLDNOIKKOLAD 764
 Qy 720 IOTKSQOIQOMADKILEBEKREAOVSAOHLFVHLKOKEOHYEEKIKVLDNOIKKOLAD 779
 Db 720 IOTKSQOIQOMADKILEBEKREAOVSAOHLFVHLKOKEOHYEEKIKVLDNOIKKOLAD 779
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 Db 765 KETLENMQRHEEBAHEKGI1SEOKAMINAMDSK1RSLRQ1VLELSEANKLAANSFLT 824
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 Db 825 QRYMKAQOEMIS1SLBOOKYLETQAGKLEAONKLEBOLEK1SHOHSIDKNLLEETRL 884
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 Db 885 REVSLEHEBOKLEKXOLTELOSLQERESQ1FALAAAPALAESOLROAKTELEETTAZ 944
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 Db 900 REVSLEHEBOKLEKXOLTELOSLQERESQ1FALAAAPALAESOLROAKTELEETTAZ 959
 Qy 945 EEB1QALTAHDE1QORFPA1RNSCTV1TDLBEOLNQLTEDNAELNNOVFYLSKQDEAS 1004
 Db 945 EEB1QALTAHDE1QORFPA1RNSCTV1TDLBEOLNQLTEDNAELNNOVFYLSKQDEAS 1004
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 Db 1005 GANDEIVOLRSEVDH1RREITEREMQ1TSQOMELKTTCTMLLEBQVMDLELNBELLE 1064
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 Db 1065 KEROMEAMSVLGDSEKSOFECEVRLEORMDTEKOSRARADORTSSROVVELAVKXHA 1124

Db 1080 KEROMEAMSVLGDSEKSOFECEVRLEORMDTEKOSRARADORTSSROVVELAVKXHA 1139
 Qy 1125 E1IALQOALKEQK1RAES1SDK1LNDLEKXAMLENNARSLOOKLETERELKORLLEBOAK 1184
 Db 1140 E1IALQOALKEQK1RAES1SDK1LNDLEKXAMLENNARSLOOKLETERELKORLLEBOAK 1199
 Qy 1185 LOOQMDLOKNH1FRLTOGLQELADBLKTERSDLEVOLENIQVLYSHEKVMETTSQ 1244
 Db 1200 LOOQMDLOKNH1FRLTOGLQELADBLKTERSDLEVOLENIQVLYSHEKVMETTSQ 1259
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 Qy 1305 LOKTRIELASAREEAAHRAKATHPHSPATARQO1MGA1YRSPBHOASMSLAPPS 1364
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 Qy 1365 RRKESSTPEEFSRRLKERMHNI1PHRFNVGLNMRATKCAVCLDTHFGRQASKECQVM 1424
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 Db 1485 GOOGMDRK1YVEGSKV1LYDNEAREAGORPVEEBELCLPDGDVSIHGAVGSELANTAK 1544
 Qy 1545 A-----EKAEDATL 1554
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 Db 1605 LGNSLLKLEGGDRDLNMC1LTPESDQV1VGTBEGYALANVLKNS1THVPGICAVPQ1Y11 1664
 Qy 1615 KOLEKLM1AGEBRALCLVDYKVKVQSLAOSH1PAQOPDISPNI1FAVKGC1HFGAKTEN 1674
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 Db 1725 GLC1CAMPKSV1LYRNMEN1SKYCIKRE1ETSEBSC1H1FTNYSL1GTNKFEYIDMKO 1784
 Qy 1735 YTLLEFLDKNDHSLAPAVPAASNSFPVSIYOVNSAGOREEYL1CFHERGVFVDSYGRS 1794
 Db 1785 YTLLEFLDKNDHSLAPAVPAASNSFPVSIYOVNSAGOREEYL1CFHERGVFVDSYGRS 1844
 Qy 1795 RTDDLKMSRLPLAFAYREBYLFTYHNSLEVE1E1OARSSAGTPADAYLD1PNRYLGPAT 1854
 Db 1845 RTDDLKMSRLPLAFAYREBYLFTYHNSLEVE1E1OARSSAGTPADAYLD1PNRYLGPAT 1904
 Qy 1855 SSGATY1LASSYODK1RV1CCKN1LVKESGTEHHRBPSTSRSSPNRGPRTVNEHTTKRA 1914
 Db 1905 SSGATY1LASSYODK1RV1CCKN1LVKESGTEHHRBPSTSRSSPNRGPRTVNEHTTKRA 1964
 Qy 1915 SSPAPPEGSHPRESTPHRYREGRTEL1RDKSPRPLEREKSPGRMLSTRERSPGRLF 1974
 Db 1965 SSPAPPEGSHPRESTPHRYREGRTEL1RDKSPRPLEREKSPGRMLSTRERSPGRLF 2024
 Qy 1975 EDSRGR1LPAGAVRTPLSQVNGKQOASQV 2005
 Db 2025 EDSRGR1LPAGAVRTPLSQVNGKQOASQV 2055

RESULT 9
 US-09-964-956-11
 ; Sequence 11, Application US/09964956
 ; Publication No. US20040043926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerlach, Valerie L

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/ APPLICANT: MacDougall, John R
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Stone, David
/ APPLICANT: Gunther, Erik
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Grose, William M
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Lepley, Denise M
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Padigar, Muralidhara
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Leach, Martin D
/ APPLICANT: Shinkets, Richard A
/ TITLE OF INVENTION: No. US20040043926A1el Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-124
/ CURRENT APPLICATION NUMBER: US/09/964,956
/ CURRENT FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 60/235,631
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/235,633
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/235,808
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/236,064
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/236,065
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/236,066
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/236,135
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: 60/237,434
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/238,321
/ PRIOR FILING DATE: 2000-10-05
/ PRIOR APPLICATION NUMBER: 60/238,399
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 60/238,396
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 60/276,667
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/294,823
/ PRIOR FILING DATE: 2001-05-31
/ PRIOR APPLICATION NUMBER: 60/304,868
/ PRIOR FILING DATE: 2001-07-12
/ NUMBER OF SEQ ID NOS: 127
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 11
/ LENGTH: 2053
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-964-956-11

Query Match      95.4%; Score 10005; DB 11; Length 2053;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1978; Conservative 3; Mismatches 5; Indels 82; Gaps 4;
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241 GSAATGNENKYNNAALPIGTPDYMAPEVLTWNNGGKTYGDCDMSVGVAYEMYGR 300
Db
241 GSAATGNENK-NVNAALPIGTPDYMAPEVLTWNNGGKTYGDCDMSVGVAYEMYGR 299
QY
301 SPFAEGTSARPTNNIMNFQFLKFPDDPKVSDFDLIQSLLCGQERLKFCGHPFF 360
Db
300 SPFAEGTSARPTNNIMNFQFLKFPDDPKVSDFDLIQSLLCGQERLKFCGHPFF 359
QY
361 SKIDWNINRNSPPFPVPTLKSDDTSNFDEPEKNSWSSSPCCPSPGSGEELPFVGRS 420
Db
360 SKIDWNINRNPAPPFPVPTLKSDDTSNFDEPEKNSWSSSPCCPSPGSGEELPFVGRS 419
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421 YKALGILIGRSSVYSGLDSPAKTSMERKLLIKSKELQDSQDKHKEQENTRLHRRVS 480
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Db
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Db
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Db
1020 GANDEIYOLRSEVDHLREITEREMQUTSOKQYMEALKTTCMTLBEQVWDEALDELLE 1079
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1065 KERQWEANRSLVGDSEKQFECRVRELQRMLDTEKQSRARADQRTIESQVVELAVKEHA 1124
Db
1080 KERQWEANRSLVGDSEKQFECRVRELQRMLDTEKQSRARADQRTIESQVVELAVKEHA 1139
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Db
1140 ETLALQALKEQKLAESLSDKLNDLEKGMLENNASLQOKLETREBELKORLLEBOAK 1199
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1185 LQQQMDLQKNHIFRLTOGLQZALDRADLLKTERSDLEFQLENIQVLYSHKRYKMGTTISQ 1244
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1260 QTKLIDFLQAKMDQPAKKKK-----VPLQYNELKLALEKARCALEBEA 1304
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DB 1305 LOKTRIELSAPBEAHRKATDHPSTPATAPQIAMSATVSPBHOBSAMLLAPSS 1364
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QY 1905 SSGATYLAASYODKLVICCKGLVKESTGHEHHRGTSRSSPNKRGPTTYNEHTKRYA 1964
DB 1905 SSGATYLAASYODKLVICCKGLVKESTGHEHHRGTSRSSPNKRGPTTYNEHTKRYA 1964
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DB 1975 EDSRGRRLPAGAVRTPLSQVNRKRGOSA 2002
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DB 2025 EDSRGRRLPAGAVRTPLSQVNRKRGOSA 2052

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RESULT 10
US-10-262-511-2 ;

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; Sequence 2, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Milet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jinfang
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Szytek, Kimberly A.
; APPLICANT: Edinger, Shiomit R.
; APPLICANT: Ellemann, Karen
; APPLICANT: Malysankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda

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; APPLICANT: Zeihusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Caterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol B. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuroSeqdlet version 0.1
; SEQ ID NO 2
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-262-511-2

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Query Match 95.4%; Score 10005; DB 15; Length 2053;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1978; Conservative 3; Mismatches 5; Indels 82; Gaps 4;

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QY 1 MLKFKYGANPLDAGAAEPIASRASRLNLFPGKPEPMTQQQMSPLSRGGIIDLAFVLE 60
DB 1 MLKFKYGANPLDAGAAEPIASRASRLNLFPGKPEPMTQQQMSPLSRGGIIDLAFVLE 60
QY 61 ECGOPALMKIKIVSNVRKYSSTIAELQLOPSADQFEVRSVYGCCHFAEVQVVRKATG 120
DB 61 ECGOPALMKIKIVSNVRKYSSTIAELQLOPSADQFEVRSVYGCCHFAEVQVVRKATG 120
QY 121 DIYAMKVMKKALLAQEOVSFFEEERNILSRSTSPMIPOLQYAFODKHLVLMEEQOPG 180
DB 121 DIYAMKVMKKALLAQEOVSFFEEERNILSRSTSPMIPOLQYAFODKHLVLMEEQOPG 180
QY 181 DLISLNRVEDQUDENLQFYLAELILAVSHVLMGVYARDIKPENILVDRGTGILVDF 240
DB 181 DLISLNRVEDQUDENLQFYLAELILAVSHVLMGVYARDIKPENILVDRGTGILVDF 240
QY 241 GSAAKKNSKVMNAKLPITGPTVMAPEVTVNNGSGKGYGIDCDQMSVGVAYENIYGR 300
DB 241 GSAAKKNSK-VNAKLPITGPTVMAPEVTVNNGSGKGYGIDCDQMSVGVAYENIYGR 299
QY 301 SPPAEGTSARTNNINMFORFLKFPDDPKVSDPLDLIGSLCGQKERLKFGLCCHPFF 360

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Db 300 SPFAEGSATFNNIMNFQRFLLKFPDDPKVSSDFLLIQSLLCGQERLKFEGLCCHPFF 359
Qy 361 SKIDMNNIRNRPFPVPTLLKSDDDTGNFDPENKSNWSSPQCLSPGSGGEBLPTVGVNS 420
Db 360 SKIDMNNIRNRPFPVPTLLKSDDDTGNFDPENKSNWSSPQCLSPGSGGEBLPTVGVNS 419
Qy 421 YSKALGILGRSESVGLDSPAKTSSMEKLLIKSKELQDSODKCHMEQEMRLRRYS 480
Db 420 YSKALGILGRSESVGLDSPAKTSSMEKLLIKSKELQDSODKCHMEQEMRLRRYS 479
Qy 481 EYVAIVISQKEVELKASSTORSLLLEODLATTYTECSSLKSLEQARMESQEDDKALQLH 540
Db 480 EYVAIVISQKEVELKASSTORSLLLEODLATTYTECSSLKSLEQARMESQEDDKALQLH 539
Qy 541 DIREOSRKLOEIKEOEQVQAVEEMRLMMQLEEDLVASARRSPLYSSELRESLAEERK 600
Db 540 DIREOSRKLOEIKEOEQVQAVEEMRLMMQLEEDLVASARRSPLYSSELRESLAEERK 599
Qy 601 RKATECOHKLKAKDOGKPEVGEYAKLEKINAEQQLKIOELQKLEKA----- 648
Db 600 RKATECOHKLKAKDOGKPEVGEYAKLEKINAEQQLKIOELQKLEKAKVASTAETELLQ 659
Qy 649 ----AERABRELKQONRDESGIRKKLVAEERHSLLENKVKLETMERRENKLKD 704
Db 660 NIRAOKARERLEKLONERDESSEGIRKKLVAEERHSLLENKVKLETMERRENKLKD 719
Qy 705 IOTKSQOIQOMADKILEBEKREAVSNQHLVHKKOEQYHEEKIKYLDNQIKKDLAD 764
Db 720 IOTKSQOIQOMADKILEBEKREAVSNQHLVHKKOEQYHEEKIKYLDNQIKKDLAD 779
Qy 765 KETLENMORHEBEAHEKGLISEQKAMINAMDSKISRLEQRIVELSEANKLAANSFLT 824
Db 780 KETLENMORHEBEAHEKGLISEQKAMINAMDSKISRLEQRIVELSEANKLAANSFLT 839
Qy 825 QNNMKAQEMISLROQKYLETQAGKLEAONRKLEBOLEKISHODHSQKRLLEETPL 884
Db 840 QNNMKAQEMISLROQKYLETQAGKLEAONRKLEBOLEKISHODHSQKRLLEETPL 899
Qy 885 REVSLHEBQKLEKROKTELQLOESRESQLTALQAPARALSESQROKKTLEETPL 944
Db 900 REVSLHEBQKLEKROKTELQLOESRESQLTALQAPARALSESQROKKTLEETPL 959
Qy 945 EEEIQAALYAHDEIQORFQALNSCTVITDLBEQNLQTEDNAELNNQNFYLSKQLEAS 1004
Db 960 EEEIQAALYAHDEIQORFQALNSCTVITDLBEQNLQTEDNAELNNQNFYLSKQLEAS 1019
Qy 1005 GANDEIVQARSEVNDHRRRITEREMQTSQKQTMALKTTCTMLBEOVMDLALDELIE 1064
Db 1020 GANDEIVQARSEVNDHRRRITEREMQTSQKQTMALKTTCTMLBEOVMDLALDELIE 1079
Qy 1065 KERQWEAMRSVLGDEKSGFECHRELQRMJLDEKOSBARADQRTIESRQVVELAYKEHA 1124
Db 1080 KERQWEAMRSVLGDEKSGFECHRELQRMJLDEKOSBARADQRTIESRQVVELAYKEHA 1139
Qy 1125 ELIALQALKEQKLAESISDKLNDLEKKHAMLENNARSLQOKLETREBLKORLLEBQAK 1184
Db 1140 ELIALQALKEQKLAESISDKLNDLEKKHAMLENNARSLQOKLETREBLKORLLEBQAK 1199
Qy 1185 LQQQMDLQKNHIFRLTQGLQEALDRAADLLKTRSLLEYOLENIQVLYSHKRYMGGTISQ 1244
Db 1200 LQQQMDLQKNHIFRLTQGLQEALDRAADLLKTRSLLEYOLENIQVLYSHKRYMGGTISQ 1259
Qy 1245 QTKLIDFLQAKMDQPAKKKGLFSRRKEDPALPTQVPLQVYNLKLALKEKARCALEBEA 1304
Db 1260 QTKLIDFLQAKMDQPAKKKGLFSRRKEDPALPTQVPLQVYNLKLALKEKARCALEBEA 1304
Qy 1305 LQKTRIEIRSAFEZAAHRAVTDHPHSTPATARQOIAWSAIVRSBEHOPSAWSLAPPS 1364
Db 1305 LQKTRIEIRSAFEZAAHRAVTDHPHSTPATARQOIAWSAIVRSBEHOPSAWSLAPPS 1364
Qy 1365 RKKESTTEBFSRRLKERHNNHIIHRFVNGLMARATKCAVCLDTVHFGROASKCLECOVM 1424

Db 1365 RKKESTTEBFSRRLKERHNNHIIHRFVNGLMARATKCAVCLDTVHFGROASKCLECOVM 1424
Qy 1425 CHPKCSTCLPATCGIPAEYATHFTPAFCBDKNSVGLQTEPSSSLHLEGMKVPRNNKR 1484
Db 1425 CHPKCSTCLPATCGIPAEYATHFTPAFCBDKNSVGLQTEPSSSLHLEGMKVPRNNKR 1484
Qy 1485 GQOGMDRKTYLEGSKVLIYDNEARAGORPVEEBELCLPDGDVSIHGAVGASELANYAK 1544
Db 1485 GQOGMDRKTYLEGSKVLIYDNEARAGORPVEEBELCLPDGDVSIHGAVGASELANYAK 1544
Qy 1545 A-----EKAEDAKL 1554
Db 1545 ADVPYILKMHESHPTTCWPGRTLYLLAPSPPDKQWMTALBSVAGRVSRKADAKL 1604
Qy 1555 LGNSLLKLEGGDRLLDMNCTLPSPDOYVLVGBEGYALANVLKNSLTHYPGIGAVQIYII 1614
Db 1605 LGNSLLKLEGGDRLLDMNCTLPSPDOYVLVGBEGYALANVLKNSLTHYPGIGAVQIYII 1664
Qy 1615 KDLKELMIAGERALCLVDYKVKVQSLAQSHLPAQPDISPNIPEAVRGCHLFGAGKLEN 1674
Db 1665 KDLKELMIAGERALCLVDYKVKVQSLAQSHLPAQPDISPNIPEAVRGCHLFGAGKLEN 1724
Qy 1675 GLCICAMPKSVVILRYNENLSKYCIRKEIETSEBSCSIHFNTYSILIGTKKFEYIDMKO 1734
Db 1725 GLCICAMPKSVVILRYNENLSKYCIRKEIETSEBSCSIHFNTYSILIGTKKFEYIDMKO 1784
Qy 1735 YTLFEPLDKNDHSLAPANFAASNSFPVSIYQVNSAGQREBYLLCFHEFGVFDVSYGRS 1794
Db 1785 YTLFEPLDKNDHSLAPANFAASNSFPVSIYQVNSAGQREBYLLCFHEFGVFDVSYGRS 1844
Qy 1795 RTDLMKMSRLPLAFAYREPLYFVTHFNLSLEYIEIQARSAGTPARAYVDINPRTYIGPAI 1854
Db 1845 RTDLMKMSRLPLAFAYREPLYFVTHFNLSLEYIEIQARSAGTPARAYVDINPRTYIGPAI 1904
Qy 1855 SSGAIYLAASYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGCPPTYNEHITKVA 1914
Db 1905 SSGAIYLAASYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGCPPTYNEHITKVA 1964
Qy 1915 SSPAPBEGSPHRESPTHRRRERGTBLRPRKSGRPLERKSGRMISTREBSFGRLF 1974
Db 1965 SSPAPBEGSPHRESPTHRRRERGTBLRPRKSGRPLERKSGRMISTREBSFGRLF 2024
Qy 1975 EDSRGRPLPAGAVTPTLSQVANKRGQSA 2002
Db 2025 EDSRGRPLPAGAVTPTLSQVANKRGQSA 2052

RESULT 11
US-10-017-216-4
; Sequence 4, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPPELBER-LIBERMAN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prot
; FILE REFERENCE: 10147-5701
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US/10/017, 216
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2055
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-017-216-4

Query Match 92.0%; Score 9656; DB 13; Length 2055;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 1903; Conservative 41; Mismatches 42; Indels 84; Gaps 5;
Qy 1 MLKFKYGARNPLDAGAAPIASRASRLNLFPOGKPPMTQOQMSPLSREGILDALFVLFE 60

Db 1 MLKFKGVNRPBASASEPIASASRLNLFQCKPPLMTQOQOQASLSREGMDALPALRE 60
 Qy 61 ECGOPALMKIKIVSNVNRKYSOTLAELOLQSPAKOPEVRSVGVCGHFAEVQVREKATG 120
 Db 61 ECGOPALMKIKIVSNVNRKYSOTLAELOLQSPAKOPEVRSVGVCGHFAEVQVREKATG 120
 Qy 121 DYAMVVMKKKALLAQEOVSFPEEBRNILSRSTSPMIPOLQVAFODKMLYLMEEQOPG 180
 Db 121 DYAMVVMKKKALLAQEOVSFPEEBRNILSRSTSPMIPOLQVAFODKMLYLMEEQOPG 180
 Qy 181 DLSLNLRYEDOLIDENTIOFYLAELILAVSHVLMGVHRDIPKENILVDRTHIKLVF 240
 Db 181 DLSLNLRYEDOLIDENTIOFYLAELILAVSHVLMGVHRDIPKENILVDRTHIKLVF 240
 Qy 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDWMVGVIAVEM1YGR 300
 Db 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDWMVGVIAVEM1YGR 300
 Qy 301 SEPABETSAFTNNINNFQRLKFPDDPKVSSDFLLIOSLCOQERLKFEGLCCHPFF 360
 Db 301 SEPABETSAFTNNINNFQRLKFPDDPKVSSDFLLIOSLCOQERLKFEGLCCHPFF 360
 Qy 361 SKIDMNNIRNSPPFPVPTLKSDDOTSNFDEPEKNSVSSPCQSPSGFSGEELPVPVGS 420
 Db 361 SKIDMNNIRNSPPFPVPTLKSDDOTSNFDEPEKNSVSSPCQSPSGFSGEELPVPVGS 420
 Qy 421 YSKALGILGRSESVGLDSPAKTSSMEKKL1KSKELQSDQDKHMEQEMTRLHRVS 480
 Db 421 YSKALGILGRSESVGLDSPAKTSSMEKKL1KSKELQSDQDKHMEQEMTRLHRVS 480
 Qy 481 EYEAUVLSQCEVELKASETORSLLEODLATYITECSSLSKSLBQARBEVSGEODKALQLH 540
 Db 481 EYEAUVLSQCEVELKASETORSLLEODLATYITECSSLSKSLBQARBEVSGEODKALQLH 540
 Qy 541 D1REGORKEO1KEOQYQAOVEEMRLMMNQLBEDLVASARRSDLYSESELRESLAEERF 600
 Db 541 D1REGORKEO1KEOQYQAOVEEMRLMMNQLBEDLVASARRSDLYSESELRESLAEERF 600
 Qy 601 RKATECOHKLAKOQKPEVGEYALKEKINAEQOLKIOLOEKLEKA----- 648
 Db 601 RKATECOHKLAKOQKPEVGEYALKEKINAEQOLKIOLOEKLEKA----- 648
 Qy 649 ----AKERAERLEKLONRBDSSEGRKCLVEABERPHSLENKVKLETMERRENKLOD 704
 Db 649 ----AKERAERLEKLONRBDSSEGRKCLVEABERPHSLENKVKLETMERRENKLOD 704
 Qy 705 IOTKSQOIQOMADKILLEEKGHEAQSQHLVHLKQKQHYEEKIKYLDNQIKKDLAD 764
 Db 705 IOTKSQOIQOMADKILLEEKGHEAQSQHLVHLKQKQHYEEKIKYLDNQIKKDLAD 764
 Qy 765 KETLEMMORHEEAEHEKILSEQKAMINAMSKIRLEQRIVEKSEANKLANSSLT 824
 Db 765 KETLEMMORHEEAEHEKILSEQKAMINAMSKIRLEQRIVEKSEANKLANSSLT 824
 Qy 825 QGRMKAOEEMISELROQKFYLETQAGKLEAONKLEBOLEKISHODSDKNLLLELETL 884
 Db 825 QGRMKAOEEMISELROQKFYLETQAGKLEAONKLEBOLEKISHODSDKNLLLELETL 884
 Qy 885 REVSLEHEBOKLEKQOLTELQSLQERSQLTALQAAAPALLESQROAKTELEETTA 944
 Db 885 REVSLEHEBOKLEKQOLTELQSLQERSQLTALQAAAPALLESQROAKTELEETTA 944
 Qy 945 EEBIQALTARDEIQKFDALRNSCTVITDLSEQLNQLTEDNAELNNQNFYLSKQDEAS 1004
 Db 945 EEBIQALTARDEIQKFDALRNSCTVITDLSEQLNQLTEDNAELNNQNFYLSKQDEAS 1004
 Qy 1005 GANDEIVOLRSEVDHLRREITEREMQTSQKQTEALKTTCTMLEBQVNDLEALNDELLE 1064
 Db 1005 GANDEIVOLRSEVDHLRREITEREMQTSQKQTEALKTTCTMLEBQVNDLEALNDELLE 1064
 Qy 1020 GANDEIVOLRSEVDHLRREITEREMQTSQKQTEALKTTCTMLEBQVNDLEALNDELLE 1079
 Db 1020 GANDEIVOLRSEVDHLRREITEREMQTSQKQTEALKTTCTMLEBQVNDLEALNDELLE 1079
 Qy 1065 KERQWAMNSVLDSEKQFECRAREIQMLDTEKORAPADQRTTSRQVVELAVEHKA 1124
 Db 1065 KERQWAMNSVLDSEKQFECRAREIQMLDTEKORAPADQRTTSRQVVELAVEHKA 1124

Db 1080 KERQWAMNSVLDSEKQFECRAREIQMLDTEKORAPADQRTTSRQVVELAVEHKA 1139
 Qy 1125 ETLAQALKEQKRAESLSDTLNLEKHALEMMANSLQOKLETERLKOILREOAK 1184
 Db 1140 ETLAQALKEQKRAESLSDTLNLEKHALEMMANSLQOKLETERLKOILREOAK 1199
 Qy 1185 LQOQMDLOKNIHFLRTOGLQALADRADLKTERRSLEYOLENIQVLYSHEKYMESTISO 1244
 Db 1200 LQOQMDLOKNIHFLRTOGLQALADRADLKTERRSLEYOLENIQVLYSHEKYMESTISO 1259
 Qy 1245 QTKLIDFLOAKKDQPAKXXXXGFSRRKEDPALPTQVPLQYNELKLALEKARCALEBA 1304
 Db 1260 QTKLIDFLOAKKDQPAKXXXXGFSRRKEDPALPTQVPLQYNELKLALEKARCALEBA 1304
 Qy 1305 LOKTRIELRSABEBAHRAKATHTHPSTPATRQOIMASAIYRSPEHOSAMSLAPSS 1364
 Db 1305 LOKTRIELRSABEBAHRAKATHTHPSTPATRQOIMASAIYRSPEHOSAMSLAPSS 1364
 Qy 1365 RRKESSTPEEFSRRILKERMHNIHPRFNVGLMRAATKCAVCLDTYHFGRAQSKLECOYM 1424
 Db 1365 RRKESSTPEEFSRRILKERMHNIHPRFNVGLMRAATKCAVCLDTYHFGRAQSKLECOYM 1424
 Qy 1425 CHPKSTCUPATCGLPABAYATHTTEAFCDKKNASBGLQTEBSSSLHEGMMKVPRNNR 1484
 Db 1425 CHPKSTCUPATCGLPABAYATHTTEAFCDKKNASBGLQTEBSSSLHEGMMKVPRNNR 1484
 Qy 1485 GOQMDRKYTVLEGSVLYLYDNABABAGORPVEFELCLPDQDVS1HGVASSELANTAK 1544
 Db 1485 GOQMDRKYTVLEGSVLYLYDNABABAGORPVEFELCLPDQDVS1HGVASSELANTAK 1544
 Qy 1545 A-----EKAEDATL 1554
 Db 1545 A-----EKAEDATL 1554
 Qy 1555 LGNSLKLLEGDRDLDMNCTLPESDQVYLVTEEGYALANLVNLSLTHVPGIAGVPOYII 1614
 Db 1605 LGNSLKLLEGDRDLDMNCTLPESDQVYLVTEEGYALANLVNLSLTHVPGIAGVPOYII 1664
 Qy 1615 KOLEKLMITAGEBRALCLVDVKKVQSLAQSHLPAPDVISPNIFEAVKCHLPAGKIXN 1674
 Db 1665 KOLEKLMITAGEBRALCLVDVKKVQSLAQSHLPAPDVISPNIFEAVKCHLPAGKIXN 1724
 Qy 1675 GLCICAMPSKVILLRYNENLSKYCIKREIETSEPCSCIHFNYSILGTNKFYEIDMO 1734
 Db 1725 GLCICAMPSKVILLRYNENLSKYCIKREIETSEPCSCIHFNYSILGTNKFYEIDMO 1784
 Qy 1735 YTLBEFLDKNDLSLAPVPAASSNSFPVSIYVANSAGOREBYILCFHEBGFVDSYGRS 1794
 Db 1785 YTLBEFLDKNDLSLAPVPAASSNSFPVSIYVANSAGOREBYILCFHEBGFVDSYGRS 1844
 Qy 1795 RTDDLKMSRLPLAFVREBYLFTVHNSLEVIQARSAGTPARAAYLIDIPNRYIGPAI 1854
 Db 1845 RTDDLKMSRLPLAFVREBYLFTVHNSLEVIQARSAGTPARAAYLIDIPNRYIGPAI 1904
 Qy 1855 SSGAIYLAASSYODKRLVTCCKNLVYESTEHHRGPTSRSSPNKRGPTTYNEHTKRA 1914
 Db 1905 SSGAIYLAASSYODKRLVTCCKNLVYESTEHHRGPTSRSSPNKRGPTTYNEHTKRA 1964
 Qy 1915 SSPAPPEBPSHREPSHPHRY--REGRTELARDKSGRPLEBEKSGRMLSTRERSPOR 1972
 Db 1965 SSPAPPEBPSHREPSHPHRY--REGRTELARDKSGRPLEBEKSGRMLSTRERSPOR 2024
 Qy 1973 LFEDESGRRLPAGAVRTPLSQVKNKGQSGA 2002
 Db 2025 LFEDESGRRLPAGAVRTPLSQVKNKGQSGA 2054

RESULT 12
 US-10-028-946-4
 ; Sequence 4, Application US/10028946
 ; Publication No. US20020123622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YU, Xuanchuan

```

; APPLICANT: Miranda, Maricar
; APPLICANT: Fridde, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1et Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1958
; TYPE: PRF
; ORGANISM: homo sapiens
; US-10-028-946-4

Query Match      90.4%; Score 9487.5; DB 13; Length 1958;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 1877; Conservative 1; Mismatches 1; Indels 81; Gaps 3;

QY      1 MLEFKYGANPLDAGAEPIASASRLNLFQGGKPPFMTQOQMSPLREGIILDALFVLE 60
DB      1 MLEFKYGANPLDAGAEPIASASRLNLFQGGKPPFMTQOQMSPLREGIILDALFVLE 60
QY      61 ECSQPALMKIKVSNFVRKYSDTIAELOEPSAKDFEVRSLVGCHEFAEVOVREKATG 120
DB      61 ECSQPALMKIKVSNFVRKYSDTIAELOEPSAKDFEVRSLVGCHEFAEVOVREKATG 120
QY      121 DIYAMKVMKKALLAQEQVSPFEEERNILSRSTSPWIPOLQYAFODKNEHLYMEEYOPG 180
DB      121 DIYAMKVMKKALLAQEQVSPFEEERNILSRSTSPWIPOLQYAFODKNEHLYMEEYOPG 180
QY      181 DLLBLINRYEDQDENTLQFYLAELILAVHSYHLMGYVRDITKPEIILYDRGHITLQNF 240
DB      181 DLLBLINRYEDQDENTLQFYLAELILAVHSYHLMGYVRDITKPEIILYDRGHITLQNF 240
QY      241 GSAAKNNSKMNNAKLPIGTPTYMAPEVLTVMNGDGKGTGGLDCMWSVGIAYEMIYGR 300
DB      241 GSAAKNNSKMNNAKLPIGTPTYMAPEVLTVMNGDGKGTGGLDCMWSVGIAYEMIYGR 300
QY      301 SPFASTGARTNNINMFORPLKPPDDPVSSDFLDLIQSLICGQKERLKFEGLCCHPFF 360
DB      301 SPFASTGARTNNINMFORPLKPPDDPVSSDFLDLIQSLICGQKERLKFEGLCCHPFF 360
QY      361 SKIDMNNINSPFPFVLTLSKDDPTSINPDEPKNSVSSPCQLSPGSGSELPVVGFS 420
DB      361 SKIDMNNINSPFPFVLTLSKDDPTSINPDEPKNSVSSPCQLSPGSGSELPVVGFS 420
QY      421 YSKALGILGRSESVSGLDSPAKTSMKKLILKSKELODSQDKCHMQEOMTRILHRYS 480
DB      421 YSKALGILGRSESVSGLDSPAKTSMKKLILKSKELODSQDKCHMQEOMTRILHRYS 480
QY      481 EYEAVLSQKEVELKASSETORSLLEODLATYITECSSLKRSLEQAMNEVSQEDDKALQLIH 540
DB      481 EYEAVLSQKEVELKASSETORSLLEODLATYITECSSLKRSLEQAMNEVSQEDDKALQLIH 540
QY      541 DIRBOSRKLOEIKEOEYQAOVEEMRLMNNQLEEDLYSARRSDIYESELRESRLAAEFK 600
DB      541 DIRBOSRKLOEIKEOEYQAOVEEMRLMNNQLEEDLYSARRSDIYESELRESRLAAEFK 600
QY      601 RKATECOHKLAKQOGKEPEGEYAKLEKINAEOQLIOELOEKLKA----- 648
DB      601 RKATECOHKLAKQOGKEPEGEYAKLEKINAEOQLIOELOEKLKA----- 648
QY      649 ----AKERAERLEKIQNREDSSEGIIRKULVEABERRHSLNKVRLFTMERERRLKMD 704
DB      661 NIROKAEERLEKIQNREDSSEGIIRKULVEABERRHSLNKVRLFTMERERRLKMD 720
QY      705 IOTKSOQIQOMADKILIEEKREAOVASHLHKKOEHOYEEKIKYLDNOIKKDLAD 764
DB      721 IOTKSOQIQOMADKILIEEKREAOVASHLHKKOEHOYEEKIKYLDNOIKKDLAD 780
QY      765 KETLENMQRHEEAHEKGIISBQKAMINAMDSKIRISLEQRIVELSEANKLAANSLSFT 824

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DB      781 KETLENMQRHEEAHEKGIISBQKAMINAMDSKIRISLEQRIVELSEANKLAANSLSFT 840
QY      825 QNMKAQEBMISELFOQKYLETOAQKLEPAONRKLEBULEKISHODSDKNLLETRL 884
DB      841 QNMKAQEBMISELFOQKYLETOAQKLEPAONRKLEBULEKISHODSDKNLLETRL 900
QY      885 REVLSHEBQKLEKROLTELOLSQERESQTLQAARALLESQROAKTELESTBA 944
DB      901 REVLSHEBQKLEKROLTELOLSQERESQTLQAARALLESQROAKTELESTBA 960
QY      945 EEEIQALTARDEIQKFDALRNSCTVITDLEEQNLQTEDEABELANNONFYLSKQJDEAS 1004
DB      961 EEEIQALTARDEIQKFDALRNSCTVITDLEEQNLQTEDEABELANNONFYLSKQJDEAS 1020
QY      1005 GANDEIVOLRSEVHDHREBITERENQOLTSQKOTMEALTTCTMLEBOYMDLEALDELLE 1064
DB      1021 GANDEIVOLRSEVHDHREBITERENQOLTSQKOTMEALTTCTMLEBOYMDLEALDELLE 1080
QY      1065 KERQWEARSVLGDEKSPBECRVRELQRMIDTEKQSRADQRTESRQVVELAVKEXHA 1124
DB      1081 KERQWEARSVLGDEKSPBECRVRELQRMIDTEKQSRADQRTESRQVVELAVKEXHA 1140
QY      1125 EILALQALKEQKLEKASLSDKLANDLEKKHAMLENNASLOQKLETERELKORLLEBOAK 1184
DB      1141 EILALQALKEQKLEKASLSDKLANDLEKKHAMLENNASLOQKLETERELKORLLEBOAK 1200
QY      1185 LQQQMDLOQNNHIFRITQGLQALDRADLLKTERSDLEYOLENIOVLYSHBEKYMGEGTISQ 1244
DB      1201 LQQQMDLOQNNHIFRITQGLQALDRADLLKTERSDLEYOLENIOVLYSHBEKYMGEGTISQ 1260
QY      1245 OTKLIDPLQAMWDOAKKKKGLFSRKEDPALPVOYPLQVNEIKALKEKARCALEBA 1304
DB      1261 OTKLIDPLQAMWDOAKKKKGLFSRKEDPALPVOYPLQVNEIKALKEKARCALEBA 1305
QY      1305 LQKTRIEILSAREEAAHKAATDHPSTPATARQOIAASALVRSBEHOPSAMSLIAPSS 1364
DB      1306 LQKTRIEILSAREEAAHKAATDHPSTPATARQOIAASALVRSBEHOPSAMSLIAPSS 1365
QY      1365 RKESSTPEBFSRLKEEMHNHIIHRRFVNGLMRATKCAVCLDLYHFSROASKLECOVM 1424
DB      1366 RKESSTPEBFSRLKEEMHNHIIHRRFVNGLMRATKCAVCLDLYHFSROASKLECOVM 1425
QY      1425 CHPKSTCLPATCGLPAYATHFEAFCDKONNSGLQTKBPSSSLHLEGMKVPBRNKR 1484
DB      1426 CHPKSTCLPATCGLPAYATHFEAFCDKONNSGLQTKBPSSSLHLEGMKVPBRNKR 1485
QY      1485 GQCGWDRKTYIVLEGSKVLIDNEAREAGQREVEBEELCLPDGDVSIHGAVGASELIANTAK 1544
DB      1486 GQCGWDRKTYIVLEGSKVLIDNEAREAGQREVEBEELCLPDGDVSIHGAVGASELIANTAK 1545
QY      1545 A-----EKABADAKL 1554
DB      1546 ADVPIILMESHPIITTCWPGRTLYLLAPSPDKORWYALVESVAGRVSEKKEADAKL 1605
QY      1555 LGSNLSLKLEGGDRIDMNCITLPSPDOVVLVGRBEGLYALNVLKNSLTHVPGAGVAYQIYI 1614
DB      1606 LGSNLSLKLEGGDRIDMNCITLPSPDOVVLVGRBEGLYALNVLKNSLTHVPGAGVAYQIYI 1665
QY      1615 KDLKELMIAGEBERALCLVDYKVKOSIAQSHLPAQDIPSNITEAVVGCILFGAGKLEN 1674
DB      1666 KDLKELMIAGEBERALCLVDYKVKOSIAQSHLPAQDIPSNITEAVVGCILFGAGKLEN 1725
QY      1675 GLCTCAMPKSVVILRYNENISKYCIKREIETSEPCSIHTNTYSILIGTKKFEIDMKQ 1734
DB      1726 GLCTCAMPKSVVILRYNENISKYCIKREIETSEPCSIHTNTYSILIGTKKFEIDMKQ 1785
QY      1735 YTLSEFLDKNDHSLAPAVFAASSNFPVSIYOVNASAGOREEYLLCFHFRGFPVDSYGRS 1794
DB      1786 YTLSEFLDKNDHSLAPAVFAASSNFPVSIYOVNASAGOREEYLLCFHFRGFPVDSYGRS 1845
QY      1795 RTDDLKMSRLPLAAYEPFLFVTHFNSLEVIETIQASSAGCTPARAYLIDINPPLYGPAT 1854

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Db 1846 RTDCLKSRRLPLAFAYREPLYFTVHFNSELEVEIQASASGAPARAVLDIPNRYLGPAT 1905
 QY 1855 SSGAIYIASSYODKLRVYICCKGNLYKSSGTEHHRGPSTR 1894
 Db 1906 SSGAIYIASSYODKLRVYICCKGNLYKSSGTEHHRGPSTR 1945

RESULT 13

US-09-964-956-40
 ; Sequence 40, Application US/09964956
 ; Publication No. US20040043926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerlach, Valerie L
 ; APPLICANT: Macdougall, John R
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Miller, Isabelle
 ; APPLICANT: Stone, David
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Grose, William M
 ; APPLICANT: Alsbrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Szytek, Kimberly A
 ; APPLICANT: Leach, Martin D
 ; APPLICANT: Shinkete, Richard A
 ; TITLE OF INVENTION: No. US20040043926A1 Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-124
 ; CURRENT APPLICATION NUMBER: US/09/964, 956
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/235, 631
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/235, 633
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/235, 808
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236, 064
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236, 065
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236, 066
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236, 135
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 60/237, 434
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/238, 321
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/238, 399
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238, 396
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/276, 667
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/294, 823
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: 60/304, 868
 ; PRIOR FILING DATE: 2001-07-12
 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 40
 ; LENGTH: 1641
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-964-956-40

Query Match 73.6%; Score 7717.5; DB 11; Length 1641;
 Best Local Similarity 90.8%; Pred. No. 0;
 Matches 1541; Conservative 15; Mismatches 16; Indels 125; Gaps 5;

QY 374 PFVPTLKSDDDTNSPFPEPKNSWSSPCQLSPSGSGELPPVGFYSKALGILGRSES 433

Db 1 PFVPTLKSDDDTNSPFPEPKNSWSSVCQLSPSGSGELPPVGFYSKALGILGRSES 60
 QY 434 VVSGLDSPAKTSMKKLLIKSKELQDSQDKCHMEQENTRLHRRVSEVAIVSQEVEL 493
 Db 61 VVSSLDSPAKVSMKKLLIKSKELQDSQDKCHMEQENTRLHRRVSEVAIVSQEVEL 120
 QY 494 KASETORSLLEODLAIYITECSLKRSLQANRVEVQEDDKLQLLHDI REOSRKQETK 553
 Db 121 KASETORSLLEODLAIYITECSLKRSLQANRVEVQEDDKLQLLHDI REOSRKQETK 180
 QY 554 EOEVQAEVEMRLMMNQLEEDLVASARRSDLYESLRJLAEPFKRATCECHTLKA 613
 Db 181 EOEVQAEVEMRLMMNQLEEDLVASARRSDLYESLRJLAEPFKRATCECHTLKA 240
 QY 614 KQCKPEVEYATLEKINAEQOLKIQELQEKLEA-----AKAEARELI 657
 Db 241 KQCKPEVEYATLEKINAEQOLKIQELQEKLEKAKASTATELLQNTROAKERARELI 300
 QY 658 EKLQNRDESEGIKKLVAEERRHSLKVKRLTEMERENRLKDDIQTKSQIQQMD 717
 Db 301 EKLNRDESEGIKKLVAE----- 321
 QY 718 KILELEKREAVSAQHLEVHLKQEQHYEEKIKVLDNQIKKDLADKETELEMNQRRHE 777
 Db 322 ---ELEEKREAVSAQHLEVHLKQEQHYEEKIKVLDNQIKKDLADKETELEMNQRRHE 378
 QY 778 EAHKRGKILSEQAMINAMDSKIRSLRORIVELSEANKLAANSSLEFQNMKAQEEIWE 837
 Db 379 EAHKRGKILSEQAMINAMDSKIRSLRORIVELSEANKLAANSSLEFQNMKAQEEIWE 438
 QY 838 LRQCKYLETQNGKLEAQRKLEBEQLEKISHQDSYKXNRLLEFTRLEVSLSEHEQKLE 897
 Db 439 LRQCKYLETQNGKLEAQRKLEBEQLEKISHQDSYKXNRLLEFTRLEVSLSEHEQKLE 498
 QY 898 LRQCKYLETQNGKLEAQRKLEBEQLEKISHQDSYKXNRLLEFTRLEVSLSEHEQKLE 957
 Db 499 LRQCKYLETQNGKLEAQRKLEBEQLEKISHQDSYKXNRLLEFTRLEVSLSEHEQKLE 558
 QY 958 IORKFDALNSCTVITDLEEQNLQEDNABLNQNFYLSKQLEASGANDEIVQLRSEV 1017
 Db 559 IORKFDALNSCTVITDLEEQNLQEDNABLNQNFYLSKQLEASGANDEIVQLRSEV 618
 QY 1018 DILRRREITEREQNLTSQKOTMEALKTTCMLSEQVMDLALDELLEKRWBAARSVIG 1077
 Db 619 DILRRREITEREQNLTSQKOTMEALKTTCMLSEQVMDLALDELLEKRWBAARSVIG 678
 QY 1078 DEKSOPECHVRELOKRLDTEKOSRABADORTIESRQVVELAVKHEKATILALQALKEOK 1137
 Db 679 DEKSOPECHVRELOKRLDTEKOSRABADORTIESRQVVELAVKHEKATILALQALKEOK 738
 QY 1138 LVAESLSDKLNDLEKKHMLNNANSLQOKLTERBELKORLLEBQAKLQOQNDLQNHIF 1197
 Db 739 LVAESLSDKLNDLEKKHMLNNANSLQOKLTERBELKORLLEBQAKLQOQNDLQNHIF 798
 QY 1198 RLTOGLQELADPADLKTERRSDLEYOLENIQVLYSHEKRWMEGITSQOTKLIDFLQAKND 1257
 Db 799 RLTOGLQELADPADLKTERRSDLEYOLENIQVLYSHEKRWMEGITSQOTKLIDFLQAKND 858
 QY 1258 QPAKKKKGLFSRKEDPALPTQVPLQVNELKLALEKAKCALEBALQKTRIELRSARE 1317
 Db 859 QPAKKKKGLFSRKEDPALPTQVPLQVNELKLALEKAKCALEBALQKTRIELRSARE 903
 QY 1318 EAHKRAVDHPHSPATARQOIAWSAIVRSEPHQPSANSLAPSSRRKESSTPEEFGR 1377
 Db 904 EAHKRAVDHPHSPATARQOIAWSAIVRSEPHQPSANSLAPSSRRKESSTPEEFGR 963
 QY 1378 RLKERMENHNTPIHRENVGLMRAATKCAVCLDTHVHGRQASKLEQVYMCIPKSTCLPATC 1437
 Db 964 RLKERMENHNTPIHRENVGLMRAATKCAVCLDTHVHGRQASKLEQVYMCIPKSTCLPATC 1023
 QY 1438 GLPAEYATHTFAFRDKNSNGLOTKEPSSSLHLEGMKVKVRNNKRGQGGDRKYIYVE 1497

Db 1024 GLPAEYATHPTFAFCRDKONSPGLQSKPESSSLHLEGMMKVPNNKRGQGMDRKTYLVE 1083
QY 1498 GSKVLIYDNEARAGORPVEBEFELCLPDGDVSIHGA VGASELANTAKA----- 1545
Db 1084 GSKVLIYDNEARAGORPVEBEFELCLPDGDVSIHGA VGASELANTAKAVPYILKMSHP 1143
QY 1546 -----EKAEDATLGNLSILKLEGGDR 1567
Db 1144 HTTCWGRITLYLLABSPFDKORWTVLAEVVAGGVRVSRKAEADAKLGNLSLKEGGDR 1203
QY 1568 LDMNCTLPFSDQVYLVGTEBGLYALNVLNKSLTHVPGA VFOIYIILKOLEKLMTAGEE 1627
Db 1204 LDMNCTLPFSDQVYLVGTEBGLYALNVLNKSLTHVIGA VFOIYIILKOLEKLMTAGEE 1263
QY 1628 RALCLVDYKVKQSLAQSHLPAQPDVSPNIFEA VVKCCHLFGACKINGLCTCAMPSTKV 1687
Db 1264 RALCLVDYKVKQSLAQSHLPAQPDVSPNIFEA VVKCCHLFGACKINSLCTCAMPSTKV 1323
QY 1688 ILRYNENLSKYCIKRIETSEPCSCIHFTNYSILIGTNKFEYEDMKQYTLLEFLDKNDH 1747
Db 1324 ILRYNENLSKYCIKRIETSEPCSCIHFTNYSILIGTNKFEYEDMKQYTLLEFLDKNDH 1383
QY 1748 LAPAVFAASSNSFPVSIYVNSAGQREBYLCTHEFGVFDVSYGRRSTDDLKMSRLPLA 1807
Db 1384 LAPAVFAASSNSFPVSIYVNSAGQREBYLCTHEFGVFDVSYGRRSTDDLKMSRLPLA 1443
QY 1808 FAYREBYLFTVHPNLSLEVEIQA RASAGTPARAYLDIPNRYLGPRISSGAIYLAASYD 1867
Db 1444 FAYREBYLFTVHPNLSLEVEIQA RASAGTPARAYLDIPNRYLGPRISSGAIYLAASYD 1503
QY 1868 KLRVICCKGNLVKSGTEHHRGSPSTRSSPNKRGPTYNEMHTTKRVA SSPAPPEGSHPR 1927
Db 1504 KLRVICCKGNLVKSGTEHHRGSPSTRSSPNKRGPTYNEMHTTKRVA SSPAPPEGSHPR 1563
QY 1928 EESTPHRY--REGRETLRDKSPGRPLERKSPGRMLSTRRSPGRLEFESSRGLPAG 1985
Db 1564 EESTPHRYRDRGRGRTLRDKSPGRPLERKSPGRMLSTRRSPGRLEFESSRGLPAG 1623
QY 1986 AVRTPLSOVNVKRGQSA 2002
Db 1624 AVRTPLSOVNVKRWDOSS 1640

RESULT 14
US-10-017-216-5
; Sequence 5, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KABELER-LIBERMAN, Rosana
; TITLE OF INVENTION: 13445, A No. US20020160483A1el Human Myotonic Dystrophy Type Prot
; FILE OF INVENTION: Kinase and Uses Therefor
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017,216
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1641
; TYPE: PRK
; ORGANISM: Mus musculus
US-10-017-216-5

Query Match 73.6%; Score 7717.5; DB 13; Length 1641;
Best Local Similarity 90.8%; Pred. No. 0;
Matches 1441; Conservative 15; Mismatches 16; Indels 125; Gaps 5;

QY 374 PVPVLTIKSDDDTSNDEPEKSNWSSPCQLSPSGSGEELPFVGSYSKALGIIIGRSRS 433
Db 1 PVPVLTIKSDDDTSNDEPEKSNWSSPCQLSPSGSGEELPFVGSYSKALGIIIGRSRS 60
QY 434 VVSGIDSPAKTSSMEKKLIIKSKELQDSQDKHMEQEWTRLLHRRVSEVAVLQKEVEL 493

Db 61 VVSGIDSPAKTSSMEKKLIIKSKELQDSQDKHMEQEWTRLLHRRVSEVAVLQKEVEL 120
QY 494 KASERORSLEBDLATYITTECSSLRSLQAMBEVSQEDDKALQULHDIREGSRKLQIEK 553
Db 121 KASERORSLEBDLATYITTECSSLRSLQAMBEVSQEDDKALQULHDIREGSRKLQIEK 180
QY 554 EOEYQAOVBEMLMNQLBEDVLSARRSDLYESLRSRLAAEFKXKATECQKILKA 613
Db 181 EOEYQAOVBEMLMNQLBEDVLSARRSDLYESLRSRLAAEFKXKATECQKILKA 240
QY 614 KOQKPEVGEYAKLEKINAQOOLKIQLOEKLEKA-----AKXAEREL 657
Db 241 KOQKPEVGEYAKLEKINAQOOLKIQLOEKLEKAVKASTATELLQNIROMKAEAREL 300
QY 658 EKLQNREDSSBEGIRKKVLAEBERRHSLNNKYRLBTMERRENLMDIQTSQOIQQWAD 717
Db 301 EKLHNREDSSBEGIRKKVLAEB----- 321
QY 718 KLELEBEKREAOVAOHLFVHLKQEQHYEKKIVLNDQIKQULADKTELENMQRHE 777
Db 322 ---ELBEKREAOVAOHLFVHLKQEQHYEKKIVLNDQIKQULADKTESLENMQRHE 378
QY 778 EAHKRGKILSEOKAMINAMDSKIRSLBORIVELSEANKLAANSLEPTORNMKAQEMTSE 837
Db 379 EAHKRGKILSEOKAMINAMDSKIRSLBORIVELSEANKLAANSLEPTORNMKAQEMTSE 438
QY 838 LRQKFFYLETOAGKLEAONRKLEBQLEKISHQDSKRNRLLELTRLEVSLEHEQKLE 897
Db 439 LRQKFFYLETOAGKLEAONRKLEBQLEKISHQDSKRNRLLELTRLEVSLEHEQKLE 498
QY 898 LKROLTELQLSQEESSQTLQARALLESOLQAKTELETTAEAREEQAALTANDE 957
Db 499 LKROLTELQLSQEESSQTLQARALLESOLQAKTELETTAEAREEQAALTANDE 558
QY 958 IQRKFDALRNSCTVITDLEBOLNQLTEDNAEINNOFYLKQJDEASGANDIEVOLARSEV 1017
Db 559 IQRKFDALRNSCTVITDLEBOLNQLTEDNAEINNOFYLKQJDEASGANDIEVOLARSEV 618
QY 1018 DILREITEREMQLTSSQKQTEALKTCTWLEBEQVMDLEALNDELLEKROMEANRSYLG 1077
Db 619 DILREITEREMQLTSSQKQTEALKTCTWLEBEQVMDLEALNDELLEKROMEANRSYLG 678
QY 1078 DEKSOFEGRVLELOMLPTEKOSRARADORTTESQVVELAVKEKAEIILAQALKEOK 1137
Db 679 DEKSOFEGRVLELOMLPTEKOSRARADORTTESQVVELAVKEKAEIILAQALKEOK 738
QY 1138 LKASLSQKINDLEKHAMLEMNARSLOQKLETERELKQRLLEBQAKIQOQMDIQKNHIF 1197
Db 739 LKASLSQKINDLEKHAMLEMNARSLOQKLETERELKQRLLEBQAKIQOQMDIQKNHIF 798
QY 1198 RLTOGLQALDRADILKTERSDLEYOLENIOVLSHEKVKMEGTTSQCTKLIDFLQAYMD 1257
Db 799 RLTOGLQALDRADILKTERSDLEYOLENIOVLSHEKVKMEGTTSQCTKLIDFLQAYMD 858
QY 1258 QPAKKKKLFSRRKEDPALPTQVPLQVVELKLALEKEXARCALEALQKRIETLSARE 1317
Db 859 QPAKKKK-----VPLQVVELKLALEKEXARCALEALQKRIETLSARE 903
QY 1318 EAAHKKATDHPHSTPATARQOIAMSAIVRSPEHOPASMSILAPSSRRKSSSTPEBSR 1377
Db 904 EAAHKKATDHPHSTPATARQOIAMSAIVRSPEHOPASMSILAPSSRRKSSSTPEBSR 963
QY 1378 RLKERMHNNIHPHRRVNGIMRATKAVCLDVHGRQASKLEQVWCHPXCSTCLPATYC 1437
Db 964 RLKERMHNNIHPHRRVNGIMRATKAVCLDVHGRQASKLEQVWCHPXCSTCLPATYC 1023
QY 1438 GLPAEYATHPTFAFCRDKONSPGLQSKPESSSLHLEGMMKVPNNKRGQGMDRKTYLVE 1497
Db 1024 GLPAEYATHPTFAFCRDKONSPGLQSKPESSSLHLEGMMKVPNNKRGQGMDRKTYLVE 1083
QY 1498 GSKVLIYDNEARAGORPVEBEFELCLPDGDVSIHGA VGASELANTAKA----- 1545

Db 1084 GSKVLLYDNEAREAGORPVEEFELCLPDGDSVHGAVGASELANTAKADVPIILKMSHP 1143
Qy 1546 -----EKAEADATLNGSLKLEGDDR 1567
Db 1144 HTTCMPGRTLYLLAIPSPDKQWVTLAESVAVAGRVAREKAEADAKLNGSLKLEGDDR 1203
Qy 1568 LDMNCTLPSPDQVVLVGTGEGLYALNVLKSLTHVFGVIGVFOIYIILKDEKLMTAGEE 1627
Db 1204 LDMNCTLPSPDQVVLVGTGEGLYALNVLKSLTHVFGVIGVFOIYIILKDEKLMTAGEE 1263
Qy 1628 RALCLVDVKKVKSQSLAQSHLPAQPDISPNIFFAVKGCHEFGAGKIEKICICAMPSPKV 1687
Db 1264 RALCLVDVKKVKSQSLAQSHLPAQPDISPNIFFAVKGCHEFGAGKIEKICICAMPSPKV 1323
Qy 1688 ILRYNNTLSKCYCKRIETSEPCSHFTMYSTLIGTKNYEIDMQYTLDEFLDKNDHS 1747
Db 1324 ILRYNNTLSKCYCKRIETSEPCSHFTMYSTLIGTKNYEIDMQYTLDEFLDKNDHS 1383
Qy 1748 LAPAVFAASNSFPVSIIVQVNSAGOREBYLLCFHEFGVFDVSYGRSRITDCLKMSRLPLA 1807
Db 1384 LAPAVFAASNSFPVSIIVQVNSAGOREBYLLCFHEFGVFDVSYGRSRITDCLKMSRLPLA 1443
Qy 1808 FAYREBYLFVTHNSLEVIIEIQASSAGTPARAYLDPNRYLGPALISSGAIYLAASYOD 1867
Db 1444 FAYREBYLFVTHNSLEVIIEIQASSAGTPARAYLDPNRYLGPALISSGAIYLAASYOD 1503
Qy 1868 KLRVTCCKGNLVESGTEHHRGSTRSSPNKRGPTNYEHITKRVASSAPPEGSHR 1927
Db 1504 KLRVTCCKGNLVESGTEHHRGSTRSSPNKRGPTNYEHITKRVASSAPPEGSHR 1563
Qy 1928 EPSTPRY--REGRTLRDRKSPGRPLERKSPGRMLSTRERSPGRLPFDSSRGRLPAG 1985
Db 1564 EPSTPRYDRDRKTLRDRKSPGRPLERKSPGRMLSTRERSPGRLPFDSSRGRLPAG 1623
Qy 1986 AVRTPLSQVKNKGQSGA 2002
Db 1624 AVRTPLSQVKNKWQSS 1640

RESULT 15
US-09-964-956-41
Sequence 41, Application US/09964956
Publication No. US20040043926A1
GENERAL INFORMATION:
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
APPLICANT: Gunther, Erik
APPLICANT: Ellemann, Karen
APPLICANT: Grobse, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine B
APPLICANT: Padigar, Muralidhara
APPLICANT: Kekuda, Ramesh
APPLICANT: Szytek, Kimberly A
APPLICANT: Leach, Martin D
APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: No. US20040043926A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-124
CURRENT APPLICATION NUMBER: US/09/964,956
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,808
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,065

PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,135
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/237,434
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/238,321
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,399
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,396
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/276,667
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/294,823
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/304,868
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 41
LENGTH: 1597
TYPE: PRT
ORGANISM: Mus musculus
US-09-964-956-41

Query Match 71.4%; Score 7491.5; DB 11; Length 1597;
Best Local Similarity 93.1%; Pred. No. 2.2e-316;
Matches 1492; Conservative 16; Mismatches 12; Indels 83; Gaps 4;

Qy 468 MEQEMTRLRHYSEVAVATSOKEVELKASETORSLLEODLATYITCESSLKSLSEARME 527
Db 9 MEQEMTRLRHYSEVAVATSOKEVELKASETORSLLEODLATYITCESSLKSLSEARME 68
Qy 528 VSOEDDKALQLADHIREQSKLOEIKOEYQAOVEEMRLMMQLEBDLYSARRSPDLYES 587
Db 69 VSOEDDKALQLADHIREQSKLOEIKOEYQAOVEEMRLMMQLEBDLYSARRSPDLYES 128
Qy 588 ELRESRLAAEFKRAKATECOHKLAKODGKPEVGEYALTEKINABOOLKIOLEKLEK 647
Db 129 ELRESRLAAEFKRAKATECOHKLAKODGKPEVGEYALTEKINABOOLKIOLEKLEK 188
Qy 648 A-----AKERARELEKLONEDESEGRKLVAAEERHSLKLVKRL 691
Db 189 AVKASTATELLQNIROAKERARELEKLNEDSESGIKKLVAAEERHSLKLVKRL 248
Qy 692 ETMERRENRLKDDIOTKSQOIQOMADKILEBEKREAOVSAQHLVHLKQEOHYEEKI 751
Db 249 ETMERRENRLKDDIOTKSQOIQOMADKILEBEKREAOVSAQHLVHLKQEOHYEEKI 308
Qy 752 KYLDNQIKKDLADKETELENMQRHEEBAHEKGIISBOKAMINAMDSKIRSLQRIVELS 811
Db 309 KYLDNQIKKDLADKETELENMQRHEEBAHEKGIISBOKAMINAMDSKIRSLQRIVELS 368
Qy 812 EANKLAANSSTLTQNMKAQOEEMISELROQKYLTETQACKLEAQRKLEBQLEKISHOH 871
Db 369 EANKLAANSSTLTQNMKAQOEEMISELROQKYLTETQACKLEAQRKLEBQLEKISHOH 428
Qy 872 SKKNRLLEETRLREVSLHEBEQKLEKROLTELQISOERESQTLAQAARALAESQR 931
Db 429 SKKNRLLEETRLREVSLHEBEQKLEKROLTELQISOERESQTLAQAARALAESQR 488
Qy 932 QAKTELEETTAEEIEIQTALHARDEIQKPDALNSCTVITDLEBQNLQLTEDNAELNN 991
Db 489 QAKTELEETTAEEIEIQTALHARDEIQKPDALNSCTVITDLEBQNLQLTEDNAELNN 548
Qy 992 QNFYLSKQIDENSGANDIYQVRSVDHRRITREBQNLTSQKQTMALKTTCTMLEBQ 1051
Db 549 QNFYLSKQIDENSGANDIYQVRSVDHRRITREBQNLTSQKQTMALKTTCTMLEBQ 608
Qy 1052 VMDLALNDELLEKROWEAMRSVYGDEKQECVREIQRLDTREKOSRARADQRTES 1111
Db 1111 VMDLALNDELLEKROWEAMRSVYGDEKQECVREIQRLDTREKOSRARADQRTES 1111

Db 609 VLDLEALNDELLEKERQWEAMRSVLGDEKSOPECEVRLEQRMIDTEKOSRARADQRTES 668
QY 1112 ROVVELAVENKAEITLALQOALKKEOKLTKESLSDKLNDELKGMLEMMARSLQOKLETE 1171
Db 669 ROVVELAVENKAEITLALQOALKKEOKLTKESLSDKLNDELKGMLEMMARSLQOKLETE 728
QY 1172 RELKQRLLEEOAKLQOQMDLQKNNHIFRLTQGLQOALDRADLLKTERSDLEYQLENIQVLY 1231
Db 729 RELKQRLLEEOAKLQOQMDLQKNNHIFRLTQGLQOALDRADLLKTERSDLEYQLENIQVLY 788
QY 1232 SHEKVMEGTISQOQTKLIDPLQAKMDQPAKKKKGLFSRKKEPALPTQVPLQYNELKAL 1291
Db 789 SHEKVMEGTISQOQTKLIDPLQAKMDQPAKKKKGLFSRKKEPALPTQVPLQYNELKAL 833
QY 1292 EKEKACAELEBLOKTRIELRSAREEAHRKATDHPSTPATARQOIAMSAIVRSPEH 1351
Db 834 EKEKACAELEBLOKTRIELRSAREEAHRKATDHPSTPATARQOIAMSAIVRSPEH 893
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GenCore version 5.1.6
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Run on: March 2, 2005, 16:13:43 ; Search time 3079.26 Seconds

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	6159	100.0	6162	US-10-325-430-11	Sequence 11, Appl1
3	6159	100.0	6574	US-10-017-216-1	Sequence 1, Appl1
4	6159	100.0	6574	US-10-325-430-10	Sequence 10, Appl1
5	6159	100.0	6574	US-10-757-262-51	Sequence 51, Appl1
6	5666.4	92.0	6298	US-10-415-011-43	Sequence 43, Appl1
7	5661.4	91.9	6165	US-10-028-946-1	Sequence 1, Appl1
8	5661.4	91.9	6165	US-10-791-666-1	Sequence 1, Appl1
9	5651.4	91.8	8656	US-10-618-941-1	Sequence 1, Appl1
10	5631	91.4	6189	US-09-964-956-10	Sequence 10, Appl1
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12	5629.8	91.4	6201	US-09-964-956-8	Sequence 8, Appl1
13	5629.8	91.4	6201	US-10-262-511-13	Sequence 13, Appl1
14	5358	87.0	5877	US-10-028-946-3	Sequence 3, Appl1
15	5358	87.0	5877	US-10-791-666-3	Sequence 3, Appl1
16	2575.2	41.8	2896	US-10-357-930-10150	Sequence 30150, A
17	2564.8	41.6	3131	US-10-276-774-117	Sequence 137, App
18	2414	39.2	2542	US-10-262-511-7	Sequence 5, Appl1
19	2317.2	37.6	2497	US-10-262-511-5	Sequence 5, Appl1
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21	1524.2	24.7	1870	US-10-262-511-9	Sequence 9, Appl1
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ALIGNMENTS

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; Publication No. US20020160483A1
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; APPLICANT: KAPILLER-LIBERMAN, Rosana
; TITLE OF INVENTION: 13445, A No. US20020160483A1e1 Human Myotonic Dystrophy Type Pro
; TITLE OF INVENTION: Kinase and Uses Therefor
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017,216
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-216-3

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4261 TGTCAAGTATGTGTCAACCCCAAGTGTCTCAAGTGTCTCAAGCCCTGCGGCTTGGCT 4320
4321 GCTGAATATGCAACATTCACCGAGGCTTCTGCGGAGCAAAATGAAATCCCAAGT 4380
4321 GCTGAATATGCAACATTCACCGAGGCTTCTGCGGAGCAAAATGAAATCCCAAGT 4380
4381 CTCGAGACCAAGAGCCAGAGAGCTTGAACCTTGAAGAGGTGATGAGAGGCTGAGAG 4440
4381 CTCGAGACCAAGAGCCAGAGAGCTTGAACCTTGAAGAGGTGATGAGAGGCTGAGAG 4440
4441 AATTAACAAAGAGAGAGAGCTTGAACAGAGAGTACATTTGCTTGAAGAGATCAAA 4500
4441 AATTAACAAAGAGAGAGAGCTTGAACAGAGAGTACATTTGCTTGAAGAGATCAAA 4500
4501 GTCCTCATTTATGACATGAGAGCCAGAGAGCTGAGAGAGCCGCTGAGAAAGATTTGAG 4560

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Db      4501  |||...|||
Qy      4561  CTGTGCTCTCCCAACGGAGATATCTATTCATGTGTCGCTGATGCTTCCGAATCTCGA
Db      4561  CTGTGCTCTCCCAACGGAGATATCTATTCATGTGTCGCTGATGCTTCCGAATCTCGA
Qy      4621  AATACAGCCAAACAGAAAAAGAGAACTGATGCTTAACTGCTTGGAAACTCCCTGCTG
Db      4621  AATACAGCCAAACAGAAAAAGAGAACTGATGCTTAACTGCTTGGAAACTCCCTGCTG
Qy      4681  AAACTGGAAGTATGACCGTCTAGACATGAACTGACCGTGCCTTCACTAGTACAGATG
Db      4681  AAACTGGAAGTATGACCGTCTAGACATGAACTGACCGTGCCTTCACTAGTACAGATG
Qy      4741  GTGTGTGTGGGACCCGAGAGAGGGCTGTACGCTTAAATGTCTTAAAACTCCCTAAC
Db      4741  GTGTGTGTGGGACCCGAGAGAGGGCTGTACGCTTAAATGTCTTAAAACTCCCTAAC
Qy      4801  CATGTCCAGGAATTGAGAGATCTTCAAAATTTATATTAACAAGGACCTGAGAGATCTA
Db      4801  CATGTCCAGGAATTGAGAGATCTTCAAAATTTATATTAACAAGGACCTGAGAGATCTA
Qy      4861  CTCATGATAGCAGAGAGAGAGAGGCGGCACTGTGTCTTGTGAGCGTGAAGAAAGTGAAC
Db      4861  CTCATGATAGCAGAGAGAGAGAGGCGGCACTGTGTCTTGTGAGCGTGAAGAAAGTGAAC
Qy      4921  TCCCTGCGCCAGTCCCACTGCTGCTCCAGCCGCAATCTCACTCAATTTTGAAGCT
Db      4921  TCCCTGCGCCAGTCCCACTGCTGCTCCAGCCGCAATCTCACTCAATTTTGAAGCT
Qy      4981  GTCAAGGGGCTGCCATTTGTTGGGGAGGAGATTTAGAAAGGGGCTCGCATCTGTGA
Db      4981  GTCAAGGGGCTGCCATTTGTTGGGGAGGAGATTTAGAAAGGGGCTCGCATCTGTGA
Qy      5041  GCCATGCCAGCAAAAGTGTCTATTTCTGCGCTCAACAGAAACTCTGACAAATATCTGATC
Db      5041  GCCATGCCAGCAAAAGTGTCTATTTCTGCGCTCAACAGAAACTCTGACAAATATCTGATC
Qy      5101  CGGAAAGATATGAGACCTTCAAGCCCTGACAGCTGATATCACTTCACTCAATTAAGATATC
Db      5101  CGGAAAGATATGAGACCTTCAAGCCCTGACAGCTGATATCACTTCACTCAATTAAGATATC
Qy      5161  CTCATTTGAACCAATTAATTTCTACGAATATGACATGAAACAGTACACGCTCGAGAAATTC
Db      5161  CTCATTTGAACCAATTAATTTCTACGAATATGACATGAAACAGTACACGCTCGAGAAATTC
Qy      5221  CTGATTAAGATATGACATTTCTTGGCACTGCTGTGTGTTGCGGCTCTTCCAAAGCTTC
Db      5221  CTGATTAAGATATGACATTTCTTGGCACTGCTGTGTGTTGCGGCTCTTCCAAAGCTTC
Qy      5281  CCTGTCTCAATGCTGAGGTGAACAGCGAGGGGAGCGAGAGATCTATGCTGTGCTTC
Db      5281  CCTGTCTCAATGCTGAGGTGAACAGCGAGGGGAGCGAGAGATCTATGCTGTGCTTC
Qy      5341  CTTGTCTCAATGCTGAGGTGAACAGCGAGGGGAGCGAGAGATCTATGCTGTGCTTC
Db      5341  CTTGTCTCAATGCTGAGGTGAACAGCGAGGGGAGCGAGAGATCTATGCTGTGCTTC
Qy      5401  TGGAGTGTGCTTACCTTTGGCTTTTGCCTACAGAGAACTTATCTGTGTGACCACTTC
Db      5401  TGGAGTGTGCTTACCTTTGGCTTTTGCCTACAGAGAACTTATCTGTGTGACCACTTC
Qy      5461  AACTACTCTGAAGTATGATGATCAAGGAGCGCTCTCAAGAGGAGCCCTGCGCGAGCG
Db      5461  AACTACTCTGAAGTATGATGATGATCAAGGAGCGCTCTCTCAAGAGGAGCCCTGCGCGAGCG
Qy      5521  TACCTGATCATCCGAAACCGGCTACCTGTGCGCTTCCATCTTCTCAAGAGCATTTAC
Db      5521  TACCTGATCATCCGAAACCGGCTACCTGTGCGCTTCCATCTTCTCAAGAGCATTTAC
Qy      5581  TTGGGTCTCTATACAGATTAATTAAGGCTCATTTGCTGACAGGAACTCTGTGAAG
Db      5581  TTGGGTCTCTATACAGATTAATTAAGGCTCATTTGCTGACAGGAACTCTGTGAAG
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Db      5581  TTGGGTCTCTATACAGATTAATTAAGGCTCATTTGCTGACAGGAACTCTGTGAAG
Qy      5641  GATCCGAGCTGAACACACACCGGGGCGCTGTCACCTCCCGAGAGCCCAACAGCGA
Db      5641  GATCCGAGCTGAACACACACCGGGGCGCTGTCACCTCCCGAGAGCCCAACAGCGA
Qy      5701  GGCCTCAGCAGTACAGAGACATTCACAAAGCGGTGCTTCCAGCCAGCGCGCC
Db      5701  GGCCTCAGCAGTACAGAGACATTCACAAAGCGGTGCTTCCAGCCAGCGCGCC
Qy      5761  GAAAGCCGAGCCACCGCGAGAGAGCAGACACCCGCTGACCGGAGAGGAGGAGCC
Db      5761  GAAAGCCGAGCCACCGCGAGAGAGCAGACACCCGCTGACCGGAGAGGAGGAGCC
Qy      5821  GAGCTGCGAGGAGCAAGTCTTCTGCGCGCCCTGAGAGCGAGAGAGTCCCGCGCGG
Db      5821  GAGCTGCGAGGAGCAAGTCTTCTGCGCGCCCTGAGAGCGAGAGAGTCCCGCGCGG
Qy      5881  ATGCTCAGCAGCGGAGAGAGCGGCTCCCGGAGAGGCTGTTGAAGACAGAGCGGCG
Db      5881  ATGCTCAGCAGCGGAGAGAGCGGCTCCCGGAGAGGCTGTTGAAGACAGAGCGGCG
Qy      5941  CGGCTGCTGCGGAGCGGTGAGAGACCCGCTGTCAGGTGACAGGAGAGAGGAGCG
Db      5941  CGGCTGCTGCGGAGCGGTGAGAGACCCGCTGTCAGGTGACAGGAGAGAGGAGCG
Qy      6001  AGTGCCTCTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT
Db      6001  AGTGCCTCTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT
Qy      6061  GACAACTGCGAGCTTACAGTGTCTGAGATCACTGATCACTGATCACTGATCACTGAT
Db      6061  GACAACTGCGAGCTTACAGTGTCTGAGATCACTGATCACTGATCACTGATCACTGAT
Qy      6121  CAGCAGTTGAAAGTCTGTTCTGAGAACAGATTAATTC
Db      6121  CAGCAGTTGAAAGTCTGTTCTGAGAACAGATTAATTC

RESULT 2
US-10-325-430-11
; Sequence 11, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Siles-Santiago, Immaculada
; APPLICANT: Rosentfeld, Julie Bech
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; FILE REFERENCE: MP101-294PIRM
; CURRENT APPLICATION NUMBER: US/10/325,430
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6162
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6162)
US-10-325-430-11

Query Match      100.0%; Score 6159; DB 16; Length 6162;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1  ATGTTGAAGTTCAAAATATGAGCGCGGAATCTTTGATGCTGTGCTGTGAACCATTT 60
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Db 61 GCCAGCGGGCCCTCAGAGCTGATCTGTTCTTCAGGGGAAACACCCCTTATGATCA 120
QY 121 CAGCAGATGCTCTCTCTTCCGAGAGGATATTAGATGCTCTCTCTCTCTCTTGA 180
Db 121 CAGCAGATGCTCTCTCTTCCGAGAGGATATTAGATGCTCTCTCTCTCTTGA 180
QY 181 GAATGAGTCAAGCTCTGATGAAAGTTAAGCAGTGAAGCACTTTGTCCGAAATAT 240
Db 181 GAATGAGTCAAGCTCTGATGAAAGTTAAGCAGTGAAGCACTTTGTCCGAAATAT 240
QY 241 TCCGACACCATAGCTAGTTACAGAGGCTCCAGCTTCGCAAGGATCA 300
Db 241 TCCGACACCATAGCTAGTTACAGAGGCTTCAGCAAGGATCA 300
QY 301 AGTCTGTAGTGTGTGCTCACTTGTGTAAGTGCAGGTGTAAAGAGAAAGCAAGG 360
Db 301 AGTCTGTAGTGTGTGTGCTCACTTGTGTAAGTGCAGGTGTAAAGAGAAAGCAAGG 360
QY 361 GACATCTATGCTATGAAAGTGAAGAGAGGCTTTATTTGCCCCAGAGCAAGTTCA 420
Db 361 GACATCTATGCTATGAAAGTGAAGAGAGGCTTTATTTGCCCCAGAGCAAGTTCA 420
QY 421 TTTTGGAGGAGAGGAGGAAATATATCTCGAAGCAAGCCCGTGAATCCCAATTA 480
Db 421 TTTTGGAGGAGAGGAGGAAATATATCTCGAAGCAAGCCCGTGAATCCCAATTA 480
QY 481 CAGTATGCTTTAGAGCAAAATACCTTTATCTGATGAGAGATATCAGCTGAGAG 540
Db 481 CAGTATGCTTTAGAGCAAAATACCTTTATCTGATGAGAGATATCAGCTGAGAG 540
QY 541 GACTGCTGTCACTTTTGAATAGATATAGAGACCAATTAGATGAAATCCTGATCA 600
Db 541 GACTGCTGTCACTTTTGAATAGATATAGAGACCAATTAGATGAAATCCTGATCA 600
QY 601 TACCTGCTGAGCTGATTTTGGCTTCCAGAGGCTTCACTGATGAGATACGTCGA 660
Db 601 TACCTGCTGAGCTGATTTTGGCTTCCAGAGGCTTCACTGATGAGATACGTCGA 660
QY 661 GACATCAAGCTGAGAACTTCTGTTGACCGCAGAGACATCAAGCTGAGATTTT 720
Db 661 GACATCAAGCTGAGAACTTCTGTTGACCGCAGAGACATCAAGCTGAGATTTT 720
QY 721 GGAATGCGCGGAAATGAATTCAAACAGATGTGAATGCCAACTCCGATTTG 780
Db 721 GGAATGCGCGGAAATGAATTCAAACAGATGTGAATGCCAACTCCGATTTG 780
QY 781 CCGATTTACATGCTCTCTGAAGTCTGATCTGATGAAAGGAGATGAAAGGCACT 840
Db 781 CCGATTTACATGCTCTCTGAAGTCTGATCTGATGAAAGGAGATGAAAGGCACT 840
QY 841 GGGCTGAGCTGATCTGATGATGATGAGTGGGCTGATTTGCTGATGATTTA 900
Db 841 GGGCTGAGCTGATCTGATGATGATGAGTGGGCTGATTTGCTGATGATTTA 900
QY 901 TCCCTCTGCGAGAGGAACTCTGCGAGAACTTCATTAATTAATTTCAAG 960
Db 901 TCCCTCTGCGAGAGGAACTCTGCGAGAACTTCATTAATTAATTTCAAG 960
QY 961 TTTTGAATTTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Db 961 TTTTGAATTTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 TTGTTGAGGCGAG 1080
Db 1021 TTGTTGAGGCGAG 1080
QY 1081 TCTAAATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 TCTAAATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140

QY 1141 TCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Db 1141 TCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGATGAAAGCTCCGCTTTGTGGGCTTT 1260
Db 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGATGAAAGCTCCGCTTTGTGGGCTTT 1260
QY 1261 TACAG 1320
Db 1261 TACAG 1320
QY 1321 CCGTGCAG 1380
Db 1321 CCGTGCAG 1380
QY 1381 TCTGAG 1440
Db 1381 TCTGAG 1440
QY 1441 GAGTGAAG 1500
Db 1441 GAGTGAAG 1500
QY 1501 TCCCTCTGAG 1560
Db 1501 TCCCTCTGAG 1560
QY 1561 TTGAG 1620
Db 1561 TTGAG 1620
QY 1621 GATATGAG 1680
Db 1621 GATATGAG 1680
QY 1681 GTGAG 1740
Db 1681 GTGAG 1740
QY 1741 CGGAGTATCTGACGATCTGAGTGAAGAGTCTCGGCTTTGCTGAGAGATTT 1800
Db 1741 CGGAGTATCTGACGATCTGAGTGAAGAGTCTCGGCTTTGCTGAGAGATTT 1800
QY 1801 CGGAG 1860
Db 1801 CGGAG 1860
QY 1861 GTGAG 1920
Db 1861 GTGAG 1920
QY 1921 CTCGAG 1980
Db 1921 CTCGAG 1980
QY 1981 CAG 2040
Db 1981 CAG 2040
QY 2041 CGGATTTCTGAG 2100
Db 2041 CGGATTTCTGAG 2100
QY 2101 CTGAG 2160
Db 2101 CTGAG 2160
QY 2161 GAGCTGAG 2220
Db 2161 GAGCTGAG 2220
QY 2221 AAG 2280

Db	2221	AAACAGAAAGCAGCATATGAGAAAAAGATTTAAAGTTTGACAAATCAGATTAAGAAA	2280
Qy	2281	GACCTGCTGCACAAAGAGACACTGAGGAACATGATGCAGAGACAAGAGAGAGCCCAT	2340
Db	2281	GACTGGCTGCACAAAGAGACACTGAGGAACATGATGCAGAGACAAGAGAGAGCCCAT	2340
Qy	2341	GAGAAAGGGCAAAATTTCTGACCGAACAGAAAGCGATGATCATGTATGATTTCCAAATC	2400
Db	2341	GAGAAAGGGCAAAATTTCTGACCGAACAGAAAGGGATGATCATGTATGATTTCCAAATC	2400
Qy	2401	AGATCCCTGGAAACAGAGATTGTGGAACGTCTGAAGCCATTAATCTTGACGAAATATGC	2460
Db	2401	AGATCCCTGGAAACAGAGATTGTGGAACGTCTGAAGCCATTAATCTTGACGAAATATGC	2460
Qy	2461	AGCTTTTTTACCAGAAAGAACATGAAGGCCCAAGAAAGATGATTTCTGAACTCAGGCAA	2520
Db	2461	AGCTTTTTTACCAGAAAGAACATGAAGGCCCAAGAAAGATGATTTCTGAACTCAGGCAA	2520
Qy	2521	CAGAAATTTTACCTCGAGACACAGAGCTGGGAAATTGAGAGGCCAGAACCCGAAACTGAG	2580
Db	2521	CAGAAATTTTACCTCGAGACACAGAGCTGGGAAATTGAGAGGCCAGAACCCGAAACTGAG	2580
Qy	2581	GAGCAGCTTGAGAAAGATCAGCCACCAAGACCACTGTGACAAAGAAATCGGCTGCTGAAC	2640
Db	2581	GAGCAGCTTGAGAAAGATCAGCCACCAAGACCACTGTGACAAAGAAATCGGCTGCTGAAC	2640
Qy	2641	GAGACAAGATTGCGGGAAGGTGATGTATAGACACAGAGGCGAAGAACTGAGCTTAAGCC	2700
Db	2641	GAGACAAGATTGCGGGAAGGTGATGTATAGACACAGAGGCGAAGAACTGAGCTTAAGCC	2700
Qy	2701	CAGCTCACAGAGCTACAGCTTCCCTGCAGAGGCGCGATGACAGATTGACAGCCCTGAC	2760
Db	2701	CAGCTCACAGAGCTACAGCTTCCCTGCAGAGGCGCGATGACAGATTGACAGCCCTGAC	2760
Qy	2761	GCTGACGGGCGGCCCTGAGAGCCAGGTTTGCCAGGCGAAGACAGAGCTGGAAGAGATCC	2820
Db	2761	GCTGACGGGCGGCCCTGAGAGCCAGGTTTGCCAGGCGAAGACAGAGCTGGAAGAGATCC	2820
Qy	2821	ACAGCAGAAAGCTGAAGAGAGATCCAGGCACTCAGGCACTATAGATGAAATCCAGCCG	2880
Db	2821	ACAGCAGAAAGCTGAAGAGAGATCCAGGCACTCAGGCACTATAGATGAAATCCAGCCG	2880
Qy	2881	AAATTTGATGCTCTTCTGTAACAGCTGTAATCTGTAATCAAGACTGAGAGCAGCTTAAC	2940
Db	2881	AAATTTGATGCTCTTCTGTAACAGCTGTAATCTGTAATCAAGACTGAGAGCAGCTTAAC	2940
Qy	2941	CAGCTGACCGAGACAACGCTGAACTCAACCAACAAATCTTACTGTCGAAACAAATC	3000
Db	2941	CAGCTGACCGAGACAACGCTGAACTCAACCAACAAATCTTACTGTCGAAACAAATC	3000
Qy	3001	GATGAGGCTTCTGGGCGCAACGACGAGATTGTACAATCTGCGAAGTGAAGCAATTC	3060
Db	3001	GATGAGGCTTCTGGGCGCAACGACGAGATTGTACAATCTGCGAAGTGAAGCAATTC	3060
Qy	3061	CGCCGGAGATCAACGGAACGAGATGATGAGTTACGACCAAGAAAGAAACGATGAGGCT	3120
Db	3061	CGCCGGAGATCAACGGAACGAGATGATGAGTTACGACCAAGAAAGAAACGATGAGGCT	3120
Qy	3121	CTGAAGACCAAGTGCACCATCTGTGAGGAACAAGTCAATGATTTGAGAGGCCCTTAACGAT	3180
Db	3121	CTGAAGACCAAGTGCACCATCTGTGAGGAACAAGTCAATGATTTGAGAGGCCCTTAACGAT	3180
Qy	3181	GAGCTGCTAGAAAAAAGCGGCAATGTGGAGAGCCCTGAGAGAGCCTCTTGCGTATGAGAA	3240
Db	3181	GAGCTGCTAGAAAAAAGCGGCAATGTGGAGAGCCCTGAGAGAGCCTCTTGCGTATGAGAA	3240
Qy	3241	TCCAGATTGATGTGCGGTTTCAGAGACTGCAGAGATGCTGTGACACCGAGAAACAGAGC	3300
Db	3241	TCCAGATTGATGTGCGGTTTCAGAGACTGCAGAGATGCTGTGACACCGAGAAACAGAGC	3300
Qy	3301	AGGCGAGAGCGGATCAAGCGGATCAACGATCTCCGAGGTGTGAGCTGCGAGTGAAG	3360

Db	3301	AGGGCCAGAGCCCGATCAGCGATCACCAGTCTGCCAGTGTGGAGCTGGACGTGAG	3360
Qy	3361	GAGCACAAGCTGAGATTCTGCTGCTGCAAGCAGGCTCTCAAGACAGAGCTGAGGCC	3420
Db	3361	GAGCACAAGGCTGAGATTCTGCTGCTGCAAGCAGGCTCTCAAGACAGACTGAGGCC	3420
Qy	3421	GAGAGCTCTTGACAGACTCAATGACTTGGAGAAAGCATGCTTATGCTTGAATGAT	3480
Db	3421	GAGAGCTCTTGACAGAGCTCAATGACTTGGAGAAAGCATGCTATCTTGAATGAT	3480
Qy	3481	GCCGGAAGCTTACAGACAGAGCTGAGACTGAACAGAGCTCAACAGAGCTTGTGAA	3540
Db	3481	GCCCGAAGCTTACAGAGAGAGCTGAGACTGAACAGAGCTCAACAGAGCTTGTGAA	3540
Qy	3541	GAGCAAGCCAAATTACAGACGAGATGAGCTTGCAGAAAATCAATTTTCGTGACT	3600
Db	3541	GAGCAAGCCAAATTACAGACGAGATGAGCTTGCAGAAAATCAATTTTCGTGACT	3600
Qy	3601	CAGGACTCAGAGAGCTTGAATGGGCTGATCTACAGAGACAGAAAGAGTGAATTG	3660
Db	3601	CAGGACTCAGAGAGCTTGAATGGGCTGATCTACAGAGACAGAAAGAGTGAATTG	3660
Qy	3661	GAGTATCAGCTGAAAAACATTCAGGTTCTATTCTCATGAAAAGTGAAATGAGAGC	3720
Db	3661	GAGTATCAGCTGAAAAACATTCAGGTTCTATTCTCATGAAAAGTGAAATGAGAGC	3720
Qy	3721	ACTATTTCTCAACAAACCAACTCATGATTTTCTGCAAGCCAAATGACCAACTGCT	3780
Db	3721	ACTATTTCTCAACAAACCAACTCATGATTTTCTGCAAGCCAAATGACCAACTGCT	3780
Qy	3781	AAAAAGAAAAAGGGTTTATTATTTAGTCAGCGAAGAGAGCCCTGTTAACCAACAGTT	3840
Db	3781	AAAAAGAAAAAGGGTTTATTATTTAGTCAGCGAAGAGAGCCCTGTTAACCAACAGTT	3840
Qy	3841	CCTTCGAGTACATAGACTGAAGCTGGCCCTTGGAGAGAGAGAAAGTCCGCTGCAAG	3900
Db	3841	CCTTCGAGTACATAGACTGAAGCTGGCCCTTGGAGAGAGAGAAAGTCCGCTGCAAG	3900
Qy	3901	CTAGAGAGAGCCCTTCAGAGAGACCAGCTCAGGCTCCGCTCCGGCCGGAGAGAGGCTGCC	3960
Db	3901	CTAGAGAGAGCCCTTCAGAGAGACCAGCTCAGGCTCCGCTCCGGCCGGAGAGAGGCTGCC	3960
Qy	3961	CACCGCAAGCAAGGACACCCACACCCATCCACGCGACCCACCGGAGGCAAGATC	4020
Db	3961	CACCGCAAGCAAGGACACCCACACCCATCCACGCGACCCACCGGAGGCAAGATC	4020
Qy	4021	GCCATGTCGCGCATCGAGCGGTGCGACAGACACGAGCCAGTGCATAGGCTGTGGGCC	4080
Db	4021	GCCATGTCGCGCATCGAGCGGTGCGACAGACACGAGCCAGTGCATAGGCTGTGGGCC	4080
Qy	4081	CGCCATCAGCCGCAAGAGAGTCTTCACTTCAGAGGAAATTATGCGGCTCTTAAG	4140
Db	4081	CGCCATCAGCCGCAAGAGAGTCTTCACTTCAGAGGAAATTATGCGGCTCTTAAG	4140
Qy	4141	GAAAGCATGCAACCAATATTTCCACCGGATTCAGATGAGATGGAACATGCAAGCCACA	4200
Db	4141	GAAAGCATGCAACCAATATTTCCACCGGATTCAGATGAGATGGAACATGCAAGCCACA	4200
Qy	4201	AAGTGTGCTGTGTCTGAGTACCGTGCATTTTGGACGCGAGCATCCAAATGTCTGAA	4260
Db	4201	AAGTGTGCTGTGTCTGAGTACCGTGCATTTTGGACGCGAGCATCCAAATGTCTGAA	4260
Qy	4261	TGTCAAGTGAATGTTCACCCCAAGTGTCCAAGTGTTCGACGCCACTTGCGGCTTGCT	4320
Db	4261	TGTCAAGTGAATGTTCACCCCAAGTGTCCAAGTGTTCGACGCCACTTGCGGCTTGCT	4320
Qy	4321	GCTGAATATGCAACACTTCACCGAGGCTTGTGCGGAGCAAAATGAATCCCAAGT	4380
Db	4321	GCTGAATATGCAACACTTCACCGAGGCTTGTGCGGAGCAAAATGAATCCCAAGT	4380
Qy	4381	CTCCAGACCAAGAGCCAGACAGCTTGACCTTGAAGGGTGAATGAAGGTGCCACG	4440
Db	4381	CTCCAGACCAAGAGCCAGACAGCTTGACCTTGAAGGGTGAATGAAGGTGCCACG	4440

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4741 GTGTGTGGGCAACGAGAGAGGCTCTACGCTGAGTGTGAAAGATCTCCCTAAC 4800
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5821 GAGCTGCGAG 5880
5821 GAGCTGCGAG 5880
5881 ATGCTCAG 5940
5881 ATGCTCAG 5940
5941 CGGCTGCTGAG 6000
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6001 AGTGCCTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 6060
6061 GAGCACTGCGAG 6120
6061 GAGCACTGCGAG 6120
6121 CAGCAGTTGAAAGTCTGTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6180
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RESULT 3
US-10-017-216-1
; Sequence 1, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMAN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1e1 Human Myotonic Dystrophy Type Prot
; TITLE OF INVENTION: Kinase and Uses Therefor
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017,216
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-216-1

Query Match 100.0%; Score 6159; DB 13; Length 6574;
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
Matches 6159; Conservative 0; Mismatches 0

1 ATGTTGAAGTTCAATTAATGAG 60
19 ATGTTGAAGTTCAATTAATGAG 78

QY 61 GCCAGCGGCGCTCAGAGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCAA 120
Db 79 GCCAGCGGCGCTCAGAGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCAA 138
QY 121 CAGCAGATGTCCTCTCTTTTCCGAGAAAGGATATTATGATGCCCTCTTGTCTCTTTGAA 180
Db 139 CAGCAGATGTCCTCTCTTTTCCGAGAAAGGATATTATGATGCCCTCTTGTCTCTTTGAA 198
QY 181 GAATGCAGTCAAGCTGCTCTGATGAGATTAAAGCATGAGCAACTTTGTCCGGAATAT 240
Db 199 GAATGCAGTCAAGCTGCTCTGATGAGATTAAAGCATGAGCAACTTTGTCCGGAATAT 258
QY 241 TCCGACACCAATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAGGACTTCGAAGTCA 300
Db 259 TCCGACACCAATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAGGACTTCGAAGTCA 318
QY 301 AGCTCTGATGCTGTGCTCACTTTGCTGAAGTCAAGTGTAAAGAGAAAGCAACCGG 360
Db 319 AGCTCTGATGCTGTGCTCACTTTGCTGAAGTCAAGTGTAAAGAGAAAGCAACCGG 378
QY 361 GACATCATGCTTAAGAAAGTGAAGAAAGAGAGCTTTATTTGGCCCAAGAGCTTTCA 420
Db 379 GACATCATGCTTAAGAAAGTGAAGAAAGAGAGCTTTATTTGGCCCAAGAGCTTTCA 438
QY 421 TTTTGTAGAGAAAGCGGAAACATATTATCTGAAAGCAAGCCGCTGATCCCAATT 480
Db 439 TTTTGTAGAGAAAGCGGAAACATATTATCTGAAAGCAAGCCGCTGATCCCAATT 498
QY 481 CAGTATGCTTTCAAGACAAATAATCACCTTTATCTGATGAGAAATATCAGCTGAGG 540
Db 499 CAGTATGCTTTCAAGACAAATAATCACCTTTATCTGATGAGAAATATCAGCTGAGG 558
QY 541 GACTTCTGTCACTTTTGAATAGATAGAAGACAGTTAGTAAACCTGATACGTTT 600
Db 559 GACTTCTGTCACTTTTGAATAGATAGAAGACAGTTAGTAAACCTGATACGTTT 618
QY 601 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGCGTTCACTGATGAGATACGTCAG 660
Db 619 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGCGTTCACTGATGAGATACGTCAG 678
QY 661 GACATCAAGCTGAGAAACATCTCGTTGACCGCACAGACCATCAAGCTGTGATTT 720
Db 679 GACATCAAGCTGAGAAACATCTCGTTGACCGCACAGACCATCAAGCTGTGATTT 738
QY 721 GGAHTGCGCGGAAAAATGAATTCAAAACAGATGATGTAATGCCAATCCCGATTGGAGC 780
Db 739 GGAHTGCGCGGAAAAATGAATTCAAAACAGATGATGTAATGCCAATCCCGATTGGAGC 798
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Db 799 CCAAGATTACATGAGCTCTCTGAAGTGTGACTGATGTAACGGGATGGAAGAGCACTTAC 858
QY 841 GGCCTGAGCTGATGACTGATGATCAGTGGCGGTGATGCTTATGAAATGATTTATGGAGA 900
Db 859 GGCCTGAGCTGATGACTGATGATCAGTGGCGGTGATGCTTATGAAATGATTTATGGAGA 918
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Db 919 TCCCTCTTTCGAGAGGAACTCTGCTGCAAGACCTTCAATTAACATTATGATTTCCAGCG 978
QY 961 TTTTGTGAATTTTCCAGATGACCCCAAGTGAAGCTTCTTGTGATCTGATTCAAAGC 1020
Db 979 TTTTGTGAATTTTCCAGATGACCCCAAGTGAAGCTTCTTGTGATCTGATTCAAAGC 1038
QY 1021 TTGTTGTGCGGCGCAAGAAAGAGACTGAAGTTGAAGCTTTGTGTCATCTTTCTTC 1080
Db 1039 TTGTTGTGCGGCGCAAGAAAGAGACTGAAGTTGAAGCTTTGTGTCATCTTTCTTC 1098
QY 1081 TCTAAATTTGACTGGAACAACATTTGTAATCTCTCTCCCTCTGTTCCCACTCTCAAG 1140
Db 1099 TCTAAATTTGACTGGAACAACATTTGTAATCTCTCTCCCTCTGTTCCCACTCTCAAG 1158

QY 1141 TCTGACGATGACCTCCAAATTTTGAATGAACCAAGAAATTCGTGGTTTCATCTCT 1200
Db 1159 TCTGACGATGACCTCCAAATTTTGAATGAACCAAGAAATTCGTGGTTTCATCTCT 1218
QY 1201 CCGTGCAGCTGAGCCCTCAGGCTTCCGGGTGAAGAACTCCGCTTTTGGGGTTTTCG 1260
Db 1219 CCGTGCAGCTGAGCCCTCAGGCTTCCGGGTGAAGAACTCCGCTTTTGGGGTTTTCG 1278
QY 1261 TACAGAAAGCACCTGGGATTTCTTGTAGATGTAGTCTGTGTCTCGAGTCTGAGCTCC 1320
Db 1279 TACAGAAAGCACCTGGGATTTCTTGTAGATGTAGTCTGTGTCTCGAGTCTGAGCTCC 1338
QY 1321 CCTGCCAAGACTAGCTTCCATGGAAGAACTTCTCATCAAAAGCAAGCTCAAGAC 1380
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QY 1381 TCTCAGGACCAAGTGTCAAGAGATGAGAGGAAATGACCCGGTTTACATCGAGAGTCA 1440
Db 1399 TCTCAGGACCAAGTGTCAAGAGATGAGAGGAAATGACCCGGTTTACATCGAGAGTCA 1458
QY 1441 GAGTGAAGGCTGTGCTTATGTCAGAAAGAGTGAAGCTGAAGGCTCTGAGACTCAGAGA 1500
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QY 1501 TCCCTCTGAGACGAGACCTTGTACCTTACATCAAGAAATGCAATGCTTAAAGCAAGT 1560
Db 1519 TCCCTCTGAGACGAGACCTTGTACCTTACATCAAGAAATGCAATGCTTAAAGCAAGT 1578
QY 1561 TTGAGCAAGACGAGATGAGAGTGTCCAGAGAGATGCAAAAGCACTGCAGCTTCCAT 1620
Db 1579 TTGAGCAAGACGAGATGAGAGTGTCCAGAGAGATGCAAAAGCACTGCAGCTTCCAT 1638
QY 1621 GATATCAAGAGCAGAGCCGGAAGCTCCAGAAATCAAAAGCAGAGTACCAAGCTTCAA 1680
Db 1639 GATATCAAGAGCAGAGCCGGAAGCTCCAGAAATCAAAAGCAGAGTACCAAGCTTCAA 1698
QY 1681 GTGGAAGAAATGAGGTTGATGATGAATCAGTTGGAAGGATCTTGTCTAGCAAGAA 1740
Db 1699 GTGGAAGAAATGAGGTTGATGATGAATCAGTTGGAAGGATCTTGTCTAGCAAGAA 1758
QY 1741 CGAGTGAATCTTACGAATCTGAGCTGAGAGAGTCTCGGCTTGTGCTGAAGATTCAG 1800
Db 1759 CGAGTGAATCTTACGAATCTGAGCTGAGAGAGTCTCGGCTTGTGCTGAAGATTCAG 1818
QY 1801 CGGAAAGCAGCAAGATGTCAAGCATAACTGTTGAAGCTTAAAGTCAAGGAAAGCTGAA 1860
Db 1819 CGGAAAGCAGCAAGATGTCAAGCATAACTGTTGAAGCTTAAAGTCAAGGAAAGCTGAA 1878
QY 1861 GTGGAAGAAATGTGGAATCTGAGAAAGATCAATGCTGAGAGAGCTCAAAATTCAGAG 1920
Db 1879 GTGGAAGAAATGTGGAATCTGAGAAAGATCAATGCTGAGAGAGCTCAAAATTCAGAG 1938
QY 1921 CTCGAAGAAATCTGAGAAAGCTGCAAGAGAGAGCCGAGAGAGAGCTGAGAAAGCTG 1980
Db 1939 CTCGAAGAAATCTGAGAAAGCTGCAAGAGAGAGCCGAGAGAGAGCTGAGAAAGCTG 1998
QY 1981 CAGAAACGAGAGGATTTCTTCTGAAGGATCAAGAAAGAGCTGTGGAAGAGCTGAGAAAGC 2040
Db 1999 CAGAAACGAGAGGATTTCTTCTGAAGGATCAAGAAAGAGCTGTGGAAGAGCTGAGAAAGC 2058
QY 2041 CGCCATTTCTGTGAGAACCAAGTAAAGAGCTAGAGCAATGAGAGCTGAGAGAAACAGA 2100
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QY 2101 CTGAAGGATGACATCCAGACAAATTCCAAACAGATCCAGATGAGCTGATTAATTTCTG 2160
Db 2119 CTGAAGGATGACATCCAGACAAATTCCAAACAGATCCAGATGAGCTGATTAATTTCTG 2178
QY 2161 GAGCTGAGAGAGAAACATGGGAGGSCCAAGTCTCAGCCCAAGACCTTAAGAGTGCCTG 2220
Db 2179 GAGCTGAGAGAGAAACATGGGAGGSCCAAGTCTCAGCCCAAGACCTTAAGAGTGCCTG 2238
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Db 2239 AAACAGAAAGAGCAGCTATGAGGAAAATTAAGTGTGGCAATCAGATTAAGAAA 2298
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Db 2299 GACCTGGCTGACAAAGAGACATCTGAGAAATATGATGACAGACACGAGAGAGGCCAT 2358
QY 2341 GAGAAAGGCAAAATTTCTCAGCGAAACAGAAAGCGATGATCAATGCTATGATTCAGATC 2400
Db 2359 GAGAAAGGCAAAATTTCTCAGCGAAACAGAAAGCGATGATCAATGCTATGATTCAGATC 2418
QY 2401 AGATCCCTGGACAGAGATTTGGAATCTGTGAAGCCAAATTAATTTGACGCAATAGC 2460
Db 2419 AGATCCCTGGACAGAGATTTGGAATCTGTGAAGCCAAATTAATTTGACGCAATAGC 2478
QY 2461 AGTCTTTTAAACCAAGAAACATGAAAGGCCCAAGAAAGATGATTTTCTGAATCTGAGCA 2520
Db 2479 AGTCTTTTAAACCAAGAAACATGAAAGGCCCAAGAAAGATGATTTTCTGAATCTGAGCA 2538
QY 2521 CAGAAATTTTAACTGGAGACACAGGCTGGAGATGGAGGCCAGAAACGAAAACTGGAG 2580
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QY 2641 GAGACAAAGTTGGGGAGGTCACTTAAGACACAGAGACGAAACTGAGCTCAAGCCG 2700
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QY 2701 CAGCTCAAGAGTCAAGCTCTCCCTGCGAGAACGGGAGTCAAGTTGACAGCCCTGCG 2760
Db 2719 CAGCTCAAGAGTCAAGCTCTCCCTGCGAGAACGGGAGTCAAGTTGACAGCCCTGCG 2778
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Db 3199 GAGCTGCTAGAAAAAAGCGGCAAGTGGAGGCTGAGAGAGCTCTCTGGGTGATGAGAA 3258
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Db 3319 AGGCGAGAGCCGATAGCGGATCAACCGAGTCTCGCCAGGTGAGAGCTGCACTGAAG 3378
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Db 4279 TGTCAAGTATGATCAACCCCAAGTCTCAAGTCTTCCAGCCACTGCGGCTTGCT 4338
QY 4321 GCTGAATATGCAACATTTCAACGAGGCTTTCTGCGTGAACAAATGAATCTCCCAAGT 4380
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QY 4381 CTCAGACCAAGAGACCCAGAGAGCTTGAACCTGGAAGGATGATGAGGATGAGGAGG 4440
Db 4399 CTCAGACCAAGAGACCCAGAGAGCTTGAACCTGGAAGGATGATGAGGATGAGGAGG 4458

4441 AATAACAAAGAGACAGAGAGCTGGAGCAGAGATGATCTCTGGAGGGATCAAA 4500
4459 AATAACAAAGAGACAGAGAGCTGGAGCAGAGATGATCTCTGGAGGGATCAAA 4518
4501 GTCTCATTTATGACATGAGAGCAGAGAGCTGAGCAGAGCGGTGAGAGATTGAG 4560
4519 GTCTCATTTATGACATGAGAGCAGAGAGCTGAGCAGAGCGGTGAGAGATTGAG 4578
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4579 CTGTGCTTCCGAGCGGGAGTGTATCTATTGATGGTGGTGGTGGTGGTGGTGG 4638
4621 AATACAGCCAAAGCAGAGAGAGCTGATGCTAACTGCTTGGAACTCCCTGCTG 4680
4639 AATACAGCCAAAGCAGAGAGAGCTGATGCTAACTGCTTGGAACTCCCTGCTG 4698
4681 AATCTGAAAGGTGATGACCGTCTAGACATGAACTGACGCTGCTTCACTGAGCAG 4740
4699 AATCTGAAAGGTGATGACCGTCTAGACATGAACTGACGCTGCTTCACTGAGCAG 4758
4741 GTGTGTGTGGGACCGAGAGAGGCTCTAGCCCTGAAATGTCTTGAATACTCCCTAAC 4800
4759 GTGTGTGTGGGACCGAGAGAGGCTCTAGCCCTGAAATGTCTTGAATACTCCCTAAC 4818
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4819 CATGTCCAGGAATTGAGAGAGCTTCAAAATTTATATTATCAAGGACCTGAGAGAGCT 4878
4861 CTCATGATGACAGAGAGAGAGCGGGACCTGTCTTGTGAGCGTGAAGAAAGTGAACAG 4920
4879 CTCATGATGACAGAGAGAGAGCGGGACCTGTCTTGTGAGCGTGAAGAAAGTGAACAG 4938
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4939 TCCCTGGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4998
4981 GTCAAGGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
4999 GTCAAGGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5058
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5059 GCCATGCCAGCAAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5118
5101 CGAAAGAGATGAGAGCTGAGAGCCCTGAGAGCTGATGATCACTTCACTTCACTTATC 5160
5119 CGAAAGAGATGAGAGCTGAGAGCCCTGAGAGCTGATGATCACTTCACTTCACTTATC 5178
5161 CTCAATTGGAACCAATTAATTTCTACAAATGACATGAGAGAGTCAAGCTCGAGAAATTC 5220
5179 CTCAATTGGAACCAATTAATTTCTACAAATGACATGAGAGAGTCAAGCTCGAGAAATTC 5238
5221 CTGAGATGAGAGATGACATTTCTTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5280
5239 CTGAGATGAGAGATGACATTTCTTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5298
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5299 CCTGTCTCAATCTGAGAGAGTGAACAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5358
5341 CACGAATTTGAGAGTGTCTGAGATTTCTTACGAAAGAGTGAAGAGAGAGAGAGAGAGAG 5400
5359 CACGAATTTGAGAGTGTCTGAGATTTCTTACGAAAGAGTGAAGAGAGAGAGAGAGAGAG 5418
5401 TGGAGTGGCTTACCTTTGGCTTGTCTTACAGAGAACTGATCTGTTTGTGAGCCACTTC 5460
5419 TGGAGTGGCTTACCTTTGGCTTGTCTTACAGAGAACTGATCTGTTTGTGAGCCACTTC 5478
5461 AACTCACTGGAAGTATGAGATCCAGAGAGCTCTCTGAGAGAGAGAGAGAGAGAGAGAG 5520
5479 AACTCACTGGAAGTATGAGATCCAGAGAGCTCTCTCTGAGAGAGAGAGAGAGAGAGAGAG 5538

5521 TACCTGACATTCCTCCAGACCCGCGCTACCTGGGCTCTGCTGCTGCTGCTGCTGCTGCT 5580
5539 TACCTGACATTCCTCCAGACCCGCGCTACCTGGGCTCTGCTGCTGCTGCTGCTGCTGCT 5598
5581 TTGGGCTCTCTACCTGAGATTAATTAAGGCTCATTTGCTGCAAGAGAACTCTGTGAG 5640
5599 TTGGGCTCTCTACCTGAGATTAATTAAGGCTCATTTGCTGCAAGAGAACTCTGTGAG 5658
5641 GAGTCGCGACCTGAGACCAACCGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5700
5659 GAGTCGCGACCTGAGACCAACCGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5718
5701 GCGCCACCCACCTGACAGAGACATCAACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5760
5719 GCGCCACCCACCTGACAGAGACATCAACAGCGCGTGGCTTCCAGCCGAGCGCGCC 5778
5761 GAAGGCCCGACGACCCGCGAG 5820
5779 GAAGGCCCGACGACCCGCGAG 5838
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5839 GAGTCGCGAGAGACCAACCGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5898
5881 ATGCTCAAGACGCGAG 5940
5899 ATGCTCAAGACGCGAG 5958
5941 CGGCTGCTGCGAG 6000
5959 CGGCTGCTGCGAG 6018
6001 AGTGCCTCTCAAGTTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 6060
6019 AGTGCCTCTCAAGTTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 6078
6061 GACAACTGCGACGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6120
6079 GACAACTGCGACGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6138
6121 CAGCAGGTTGAAAGTCTGTTCTGAGAACAGATTATTCG 6159
6139 CAGCAGGTTGAAAGTCTGTTCTGAGAACAGATTATTCG 6177

RESULT 4
US-10-325-430-10
Sequence 10, Application US/10325430
Publication No. US20030153525A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Rosenfeld, Julie Beth
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
FILE REFERENCE: MP101-294P1RNM
CURRENT APPLICATION NUMBER: US/10/325,430
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/341,953
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 6574
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-325-430-10

Query Match 100.0%; Score 6159; DB 16; Length 6574;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2179 GAGCTCGAAGAGAAACATCGGAGAGCCCAAGTCTCAGCCGACGACTAGAAAGTGCACCTG 2238
QY 2221 AAAAGAAAGAGCGGCACTATGAGGAAAGATTAAAGTTTGAACAATTCAGATTAAGAAA 2280
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Db 2539 CAGAAATTTTAACTCTGAGAGACACAGCTGGGAGATTGAGAGCCCAAGAACCGAAAACTGAG 2598
QY 2581 GAGCAGCTGGAGAGATCAGCCACCAAGACCAAGTGAAGAAATGGGCTGGGAATCTG 2640
Db 2599 GAGCAGCTGGAGAGATCAGCCACCAAGACCAAGTGAAGAAATGGGCTGGGAATCTG 2658
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QY 2821 ACAGCGAAGCTGAGAGAGAGATCCAGGCACTCAGCGCAATAGAGATGAAATCCAGCGC 2880
Db 2839 ACAGCGAAGCTGAGAGAGAGATCCAGGCACTCAGCGCAATAGAGATGAAATCCAGCGC 2898
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RESULT 5
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 / Sequence SI, Application US/10757262
 / Publication No. US20040197825A1
 / GENERAL INFORMATION:
 / APPLICANT: Karicheh, Venkateswarlu
 / APPLICANT: Siles-Santiago, Inmaculada
 / APPLICANT: Elisabof, Scott D.
 / TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 / TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
 / TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 16405, 18560, 2047,
 / TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 51164,
 / TITLE OF INVENTION: 53010, 16852, 15887, 22072, 22245, 2387, 52908, 69112, 14990,
 / TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 23951, 2554, 8675,
 / TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
 / TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
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NUMBER OF SEQ ID NOS: 136
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 6574
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (19) ... (6180)
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Query Match 100.0%; Score 6159; DB 18; Length 6574;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3439 GAGAGCTCTGACAAAGCTCAATGACCTGAGAAAGACATGCTATGCTTGAATGAAT 3498
QY 3481 GCCCGAAGCTTACAGAGAAAGCTGAGAGATGAAACAGAGCTCAACAGAGGCTTCTGAA 3540
DB 3499 GCCCGAAGCTTACAGAGAAAGCTGAGAGATGAAACAGAGCTCAACAGAGGCTTCTGAA 3558
QY 3541 GAGCAAGCCAAATTAACAGAGAGATGAGACTGACAGAAATCAATTTCCGCTGACT 3600
DB 3559 GAGCAAGCCAAATTAACAGAGAGATGAGACTGACAGAAATCAATTTCCGCTGACT 3618
QY 3601 CAAAGACTCAAGAAAGCTTGAATCGGCTGATCTTACTGAAGACAGAAAGAGTGACTTG 3660
DB 3619 CAAAGACTCAAGAAAGCTTGAATCGGCTGATCTTACTGAAGACAGAAAGAGTGACTTG 3678
QY 3661 GAGTATCAGCTGAGAAACATTAAGGTTCTTATCTCATGAAAGGTGAATGAAAGC 3720
DB 3679 GAGTATCAGCTGAGAAACATTAAGGTTCTTATCTCATGAAAGGTGAATGAAAGC 3738
QY 3721 ACTATTCTCAACAAACCAATCATGATTTTCTGCAAGCCAAATGAGCCAACTGCT 3780
DB 3739 ACTATTCTCAACAAACCAATCATGATTTTCTGCAAGCCAAATGAGCCAACTGCT 3798
QY 3781 AAAAGAAAAAGGTTTATTTAGTGCAGGAAAGAGACCTTGCTTACCAACAGGTT 3840
DB 3799 AAAAGAAAAAGGTTTATTTAGTGCAGGAAAGAGACCTTGCTTACCAACAGGTT 3858
QY 3841 CCTCTGATTAACAATGAGTGAAGCTGAGGCTCTGAGAGAGAGAGAGAGTCTGCTGAGAG 3900
DB 3859 CCTCTGATTAACAATGAGTGAAGCTGAGGCTCTGAGAGAGAGAGAGAGTCTGCTGAGAG 3918
QY 3901 CTAGAGAAAGCCCTTCAGAAAGACCCGATCGAGCTCGGCTCGGCGGAGAGAACTGCG 3960

Db	3919	CTAGAGAAAGCCCTTCAAGAACCCGCATCGACTCCGGTCCGCCCGGAGAAAGCTCC	3978
OY	3961	CACCGCAAGCAACGAGCAACCAACCATCAAGCCAGCCACCGGAGAGATC	4020
Db	3979	CACCGCAAGCAACGAGCAACCAACCATCAAGCCAGCCACCGGAGAGATC	4038
OY	4021	GCCATTCGCGCATCGTGGGTTCGCGCAGAGCAACGACCGTAGCTCTGTGCC	4080
OY	4081	CCGCCATCCAGCCCGAGAAAGAGCTTCACTCCAGAGAAATTAGTCGGGCTTAG	4140
Db	4099	CCGCCATCCAGCCCGAGAAAGAGCTTCACTCCAGAGAAATTAGTCGGGCTTAG	4158
OY	4141	GAAACGATCACCACAAATTTCTCAACCGATTCAAGTGAATCTGAACATGCAACCA	4200
Db	4159	GAAACGATCACCACAAATTTCTCAACCGATTCAAGTGAATCTGAACATGCAACCA	4218
OY	4201	AAGTGTGCTGTGTCTGGATACGATGACCTTTGGAGCCGAGCATCCAAATGTCTGAA	4260
Db	4219	AAGTGTGCTGTGTCTGGATACGATGACCTTTGGAGCCGAGCATCCAAATGTCTGAA	4278
OY	4261	TGTCAAGTGAATGTTCACCCCAAGTGTCCAAGTCTTTCAGGCACTTCGGCTTGCCT	4320
Db	4279	TGTCAAGTGAATGTTCACCCCAAGTGTCCAAGTCTTTCAGGCACTTCGGCTTGCCT	4338
OY	4321	GCTGAATATGSCACACCTTCAACGAGGCTCTTGGCCGTGAACAAATGAATCTCCCAAGT	4380
Db	4339	GCTGAATATGSCACACCTTCAACGAGGCTCTTGGCCGTGAACAAATGAATCTCCCAAGT	4398
OY	4381	CTCCAGACCAAGAGCCCGACAGCAGCTTGCACCTGGAAGGATGAAAGTSCCAGG	4440
Db	4399	CTCCAGACCAAGAGCCCGACAGCAGCTTGCACCTGGAAGGATGAAAGTSCCAGG	4458
OY	4441	AATATCAAAACAGAGCAGCAAGAGCTGGGACAGAAATCAATTTGTCCTGAGGGATCAAA	4500
Db	4459	AATATCAAAACAGAGCAGCAAGAGCTGGGACAGAAATCAATTTGTCCTGAGGGATCAAA	4518
OY	4501	GTCCTCATTTATGACAAATGAAGCCAGAGACTGAGACAGAGCCGGTGAAGAAATTGAG	4560
Db	4519	GTCCTCATTTATGACAAATGAAGCCAGAGACTGAGACAGAGCCGGTGAAGAAATTGAG	4578
OY	4561	CTGTGACCTTCCCGACGGGAGATGATCTAATTCATGTGCGGTTGTCTCCGAATTCGCA	4620
Db	4579	CTGTGACCTTCCCGACGGGAGATGATCTAATTCATGTGCGGTTGTCTCCGAATTCGCA	4638
OY	4621	AATACAGCCAAAGCAGAAATAAGCAGAGAGCTGAACCTGAACCTCCGCTGCG	4680
Db	4639	AATACAGCCAAAGCAGAAATAAGCAGAGAGCTGAACCTGAACCTCCGCTGCG	4698
OY	4681	AAACTGGAAGGTGATGACCGCTTGAAGCATGACGCGTGCCTTCAGTGAACAGGTG	4740
Db	4699	AAACTGGAAGGTGATGACCGCTTGAAGCATGACGCGTGCCTTCAGTGAACAGGTG	4758
OY	4741	GTTGTTGGTGGCACCGAGGAAGGCTCTAGCCCTGATATCTTGAATAAATCTCCTAACC	4800
Db	4759	GTTGTTGGTGGCACCGAGGAAGGCTCTAGCCCTGATATCTTGAATAAATCTCCTAACC	4818
OY	4801	CATGTCCCAAGATTGAGCAGTCTTCAAAATTTATTTATCAAGGACCTGGAGAAAGCTA	4860
Db	4819	CATGTCCCAAGATTGAGCAGTCTTCAAAATTTATTTATCAAGGACCTGGAGAAAGCTA	4878
OY	4861	CTCATGATAGCAGGAGAAAGCCGGGCACTGTGTCTTGTGACGTGAAGAAAGTGAACAG	4920
Db	4879	CTCATGATAGCAGGAGAAAGCCGGGCACTGTGTCTTGTGACGTGAAGAAAGTGAACAG	4938
OY	4921	TCCCTGGCCAGTCCCACTGCTGCGCCACCGGACATCTCACCCAACTTTTGAAGCT	4980
Db	4939	TCCCTGGCCAGTCCCACTGCTGCGCCACCGGACATCTCACCCAACTTTTGAAGCT	4998
OY	4981	GTCAGAGGCTGCCACTTGTTTGGGACAGGCAAGTGAAGACGGGCTTGCATCTGTGCA	5040

Db	4999	GTCAAGAGGCTGCCACTTGTGTTTGGGCGACGGAAGATTGAACGGGCTGTGACTGTGCA	5051
Qy	5041	GGCATGCCAGCAAAAGTCGTCAATTCGCGCTACAACGAAACCTGACGAAATATGCAATC	5100
Db	5059	GGCATGCCAGCAAAAGTGTCAATTCGCGCTACAACGAAACCTGACGAAATATGCAATC	5113
Qy	5101	CGAAAGAGATAGAGACCTCAAGCCCTGACGTATTCACCTTACCAATTAACGATATC	5167
Db	5119	CGAAAGAGATAGAGACCTCAAGCCCTGACGTATTCACCTTACCAATTAACGATATC	5178
Qy	5161	CTCATTTGAAACCAATPAATTTCTACGAAATTCGACATGAAGAGTACACGCTCGAGGAATTC	5222
Db	5179	CTCATTTGAAACCAATPAATTTCTACGAAATTCGACATGAAGAGTACACGCTCGAGGAATTC	5233
Qy	5221	CTGGAATAGAAATGACCAATTCCTTGGCACTCTGTGTGTTCCGCTCTTCCAAACGCTTC	5280
Db	5239	CTGGAATAGAAATGACCAATTCCTTGGCACTCTGTGTGTTCCGCTCTTCCAAACGCTTC	5299
Qy	5281	CCGTACTCAATGTGACAGGTGAACAGCGACGGGCGAGAGAGGATCTGTGTGTTC	5344
Db	5299	CCGTACTCAATGTGACAGGTGAACAGCGACGGGCGAGAGAGGATCTGTGTGTTC	5355
Qy	5341	CACGAATTTGAGTGTGTGTGATTTCTTACGGAACGCTAGCCGACAGAGATCTCAAG	5400
Db	5359	CACGAATTTGAGTGTGTGTGATTTCTTACGGAACGCTAGCCGACAGAGATCTCAAG	5418
Qy	5401	TGGAATGCGCTAACCTTTGGCCCTTTGGCCCTACAGAGAACCTTATCTGTTTGAACCACTTC	5466
Db	5419	TGGAATGCGCTAACCTTTGGCCCTTTGGCCCTACAGAGAACCTTATCTGTTTGAACCACTTC	5478
Qy	5461	AACTCACTCGAAGTAATTGAGATCCAGGCACGCTCTTCAGAGAGGACCCTCGCCGAGCG	5520
Db	5479	AACTCACTCGAAGTAATTGAGATCCAGGCACGCTCTTCAGAGAGGACCCTCGCCGAGCG	5538
Qy	5521	TACCTGGAACATCCCGAACCCTCGCTACCTGAGCCCTGCAATTTCTCAGAGGCAATTAAC	5580
Db	5539	TACCTGGAACATCCCGAACCCTCGCTACCTGAGCCCTGCAATTTCTCAGAGGCAATTAAC	5598
Qy	5581	TTGGCGTCTCATATACCAAGATTAATTAAGGTCATTTGCTGTCAGAGGGAACCTGTGTAAAG	5640
Db	5599	TTGGCGTCTCATATACCAAGATTAATTAAGGTCATTTGCTGTCAGAGGGAACCTGTGTAAAG	5658
Qy	5641	GAGTCGCGGCACTGAACCAACACCGGCGCCCGCTGCACCTTCGCGACAGCCCCAACAGCGA	5700
Db	5659	GAGTCGCGGCACTGAACCAACACCGGCGCCCGCTGCACCTTCGCGACAGCCCCAACAGCGA	5718
Qy	5701	GAGCCACCAAGTAACAAGAGCAATCAACAAGGCGGTGCTCAAGCCGACGCGCCGCGCC	5760
Db	5719	GAGCCACCAAGTAACAAGAGCAATCAACAAGGCGGTGCTCAAGCCGACGCGCCGCGCC	5778
Qy	5761	GAAGGCCCCAGCAACCCGCGAGAGCAACCAACCAACGCTACCGCGAGGGCGGAGCC	5820
Db	5779	GAAGGCCCCAGCAACCCGCGAGAGCAACCAACCAACGCTACCGCGAGGGCGGAGCC	5838
Qy	5821	GAGCGTGGCGAGGAGCAAGTCTCTCGGCGCGCCCTCGAAGGAGAGAGTCCCTCGCGCGG	5880
Db	5839	GAGCGTGGCGAGGAGCAAGTCTCTCGGCGCGCCCTCGAAGGAGAGAGTCCCTCGCGCGG	5898
Qy	5881	ATGCTCTAGCAACGCGAGAGAGCGGTCCCCCGGAGGCTGTTTGAAGCACAGCAGCGGGC	5940
Db	5899	ATGCTCTAGCAACGCGAGAGAGCGGTCCCCCGGAGGCTGTTTGAAGCACAGCAGGGGC	5958
Qy	5941	CGGTCGCTCGGGGAGCGCTGAGAGATCCCGCTGTCTCCAGGTAAACAAGGAGAGGGCAG	6000
Db	5959	CGGTCGCTCGGGGAGCGCTGAGAGATCCCGCTGTCTCCAGGTAAACAAGGAGAGGGCAG	6018
Qy	6001	AGTGCCTCTCAAGTTTTCACGGTTAAACATGTACACCTATTAATGATCGGAATTAAGAGCTG	6060
Db	6019	AGTGCCTCTCAAGTTTTCACGGTTAAACATGTACACCTATTAATGATCGGAATTAAGAGCTG	6078
Qy	6061	GACAACTGCACGTAACGTGTAGTCTTGAGGATCATCCAGCTGAATGAGAGAAATCCGG	6120
Db	6079	GACAACTGCACGTAACGTGTAGTCTTGAGGATCATCCAGCTGAATGAGAGAAATCCGG	6138

QY 6121 CAGCAGGTGAAAGTCTGTTCTGAGACAGATTATTC 6159
Db 6139 CAGCAGGTGAAAGTCTGTTCTGAGACAGATTATTC 6177

RESULT 6

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TITLE OF INVENTION: HUMAN KINASES
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PRIOR APPLICATION NUMBER: US 60/249,565
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NUMBER OF SEQ ID NOS: 44
SOFTWARE: PERL Program
SEQ ID NO 43
LENGTH: 6298
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: incyte ID No. US2004053394A1 7484498CB1
US-10-415-011-43

Query Match 92.0%; Score 5666.4; DB 17; Length 6298;
Best Local Similarity 95.5%; Pred. No. 0;
Matches 5961; Conservative 0; Mismatches 36; Indels 243; Gaps 3;

QY 1 ATGTGAAGTGAATAATGAGCGCGGAATCCCTTGGATGCTGTCGTAACCCATT 60
Db 55 ATGTGAAGTGAATAATGAGCGCGGAATCCCTTGGATGCTGTCGTAACCCATT 114
QY 61 GCCAGCCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCA 120
Db 115 GCCAGCCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCA 174
QY 121 CAGCAGATGTCCTCTCTTTCCGAGAGGGAATATGATGCCCTCTTGTCTCTTTGAA 180
Db 175 CAGCAGATGTCCTCTCTTTCCGAGAGGGAATATGATGCCCTCTTGTCTCTTTGAA 234
QY 181 GAATGAGTCAGGCTGCTGATGGAAGATTAAGCAGGTGAGAACTTTGCGGAAGTAT 240
Db 235 GAATGAGTCAGGCTGCTGATGGAAGATTAAGCAGGTGAGAACTTTGCGGAAGTAT 294
QY 241 TCCGACACCATAGCTAGTTACAGAGCTCCAGCCTTCGGCAAAAGACTTCAGAGTCA 300
Db 295 TCCGACACCATAGCTAGTTACAGAGCTCCAGCCTTCGGCAAAAGACTTCAGAGTCA 354
QY 301 AGCTTTGATGTTGCTGCTCACTTTGCTGAGTGCAGTGTGTAAGAGAAAGCAACCGG 360
Db 355 AGCTTTGATGTTGCTGCTCACTTTGCTGAGTGCAGTGTGTAAGAGAAAGCAACCGG 414
QY 361 GACATCTATGCTATGAAAGTGAAGAAAGAGGCTTTATGGCCGAGAGAGGTTTCA 420
Db 415 GACATCTATGCTATGAAAGTGAAGAAAGAGGCTTTATGGCCGAGAGAGGTTTCA 474
QY 421 TTTTGTGAGGAAGAGGGAACATATATCTCAAGCAACAGCCGTGATCCCAATTA 480
Db 475 TTTTGTGAGGAAGAGGGAACATATATCTCAAGCAACAGCCGTGATCCCAATTA 534
QY 481 CAGATGCTCTTCAAGCAAAATCACTTTATCTGATGAGAGAAATATCAGCTGAGGG 540
Db 535 CAGATGCTCTTCAAGCAAAATCACTTTATCTGATGAGAGAAATATCAGCTGAGGG 594
QY 541 GACTTGTCTGCTTTTGAATATGATGAGCAAGTGTGATGAAACCTGTATACGTT 600
Db 595 GACTTGTCTGCTTTTGAATATGATGAGCAAGTGTGATGAAACCTGTATACGTT 654
QY 601 TACCTAGCTGAGCTGATTTTGGCTGTCACAGCTTCATCTGATGAGATACGTCATCA 660
Db 655 TACCTAGCTGAGCTGATTTTGGCTGTCACAGCTTCATCTGATGAGATACGTCATCA 714
QY 661 GACATCAAGCTGAGAAATCTCTGTTGACGACAGGACACATCAAGCTGTGATTTT 720
Db 715 GACATCAAGCTGAGAAATCTCTGTTGACGACAGGACACATCAAGCTGTGATTTT 774
QY 721 GATCTGCGCGGAAATGAATTCAAACAAAGATGTAATGCCAACTCCGATTGGAGC 780
Db 775 GATCTGCGCGGAAATGAATTCAAACAAAGATGTAATGCCAACTCCGATTGGAGC 834
QY 781 CCAGATTAATGATGCTCTGTAAGTGTGATGTAAGAGGGATGAAAGGACCTTAC 840
Db 835 CCAGATTAATGATGCTCTGTAAGTGTGATGTAAGAGGGATGAAAGGACCTTAC 894
QY 841 GGCCTGGAATGATGCTGCTGATGCTGATGCTGATGCTGATGATGATGATGATGATG 900
Db 895 GGCCTGGAATGATGCTGCTGATGCTGATGCTGATGCTGATGATGATGATGATGATG 954
QY 901 TCCCTCTTGGCAGAGGAACTCTGCGCAGAACTTCATTAATTAATTAATTTCCAGCG 960
Db 955 TCCCTCTTGGCAGAGGAACTCTGCGCAGAACTTCATTAATTAATTAATTTCCAGCG 1014
QY 961 TTTTGAATTTCCAGATGACCCCAAGGAGCAGTGAATTTCTTGTATCTGATCAAGC 1020
Db 1015 TTTTGAATTTCCAGATGACCCCAAGGAGCAGTGAATTTCTTGTATCTGATCAAGC 1074
QY 1021 TTGTGTGCGGCGAAGAAAGAGACTGAAGTTGAAGCTTTTGTGCTGCAATCTTTTC 1080
Db 1075 TTGTGTGCGGCGAAGAAAGAGACTGAAGTTGAAGCTTTTGTGCTGCAATCTTTTC 1134

QY	1081	TCGTAATTGACTGGAAACAACATTCGTGTAACCTCTCTCCCTCCCTTGCTTGGTTCACACCTCGAAG	1140
Db	1135	TCGTAATTGACTGGAAACAACATTCGTGTAACCTCTCCCTCCCTTGCTTGGTTCACACCTCGAAG	1194
QY	1141	TCGAGAGATGACACCTCCCAATTTTGTATGTAACAAGAAAGAAATTCGTGGGTTTCAATCCCT	1200
Db	1195	TCGAGAGATGACACCTCCCAATTTTGTATGTAACAAGAAAGAAATTCGTGGGTTTCAATCCCT	1254
QY	1201	CGGTGACAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG	1260
Db	1255	CGGTGACAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG	1314
QY	1261	TACAGCAAGGCACTGGGGATTTCTGGTGTGATCTGAGCTGTTTGTGTCTGGGTCTGAATCC	1320
Db	1315	TACAGCAAGGCACTGGGGATTTCTGGTGTGATCTGAGCTGTTTGTGTCTGGGTCTGAATCC	1374
QY	1321	CCTGCCAAGACTAGCTCCATGTGAAAAAGAACTTCTCATCAAAAGCAAAAGACTCAAGAC	1380
Db	1375	CCTGCCAAGACTAGCTCCATGTGAAAAAGAACTTCTCATCAAAAGCAAAAGACTCAAGAC	1434
QY	1381	TCTCAGGACAACTGTCCACAAGATGGAAGCAAGAAATGATCCCGTTTCACTCGAGAGTGTCA	1440
Db	1435	TCTCAGGACAACTGTCCACAAGATGGAAGCAAGAAATGATCCCGTTTCACTCGAGAGTGTCA	1494
QY	1441	GAGGTGAGGCTGTGCTTAACTCAGAAGAGGTGAGCTGAAGGCTCTGAAGACTCAGAGA	1500
Db	1495	GAGGTGAGGCTGTGCTTAACTCAGAAGAGGTGAGCTGAAGGCTCTGAAGACTCAGAGA	1554
QY	1501	TCCCTCCCTGGAGCAGAGACCTTGCTCTCACTCACTCAGATCAGTACGTTTAAACGGAAGT	1560
Db	1555	TCCCTCCCTGGAGCAGAGACCTTGCTCTCACTCACTCAGATCAGTACGTTTAAACGGAAGT	1614
QY	1561	TTGAGCAAGCAACGATGAGGTGTCCAGAGAGATGACAAAGCACTGCAGCTTCTCAT	1620
Db	1615	TTGAGCAAGCAACGATGAGGTGTCCAGAGAGATGACAAAGCACTGCAGCTTCTCAT	1674
QY	1621	GATATCAAGAGCAGAGCCCGGAAGCTCCAGAAATCAAAGACAGAGTACAGGCTCAA	1680
Db	1675	GATATCAAGAGCAGAGCCCGGAAGCTCCAGAAATCAAAGACAGAGTACAGGCTCAA	1734
QY	1681	GTGGAAGAAATGAGGTTGATGATGAAATCAGTTGGAAGAGATCTGTCTCAGCAAGAGA	1740
Db	1735	GTGGAAGAAATGAGGTTGATGATGAAATCAGTTGGAAGAGATCTGTCTCAGCAAGAGA	1794
QY	1741	CGAGATGATCTCTACGAATCTTGAAGTGAAGAGATCTTGGCTGTCTGTAAGATTCAG	1800
Db	1795	CGAGATGATCTCTACGAATCTTGAAGTGAAGAGATCTTGGCTGTCTGTAAGATTCAG	1854
QY	1801	CGAAAGAGCAGAGATGTCAAGATTAACGTGTGAAGGCTTAAGATCAAAGGAAGCCTGAA	1860
Db	1855	CGAAAGAGCAGAGATGTCAAGATTAACGTGTGAAGGCTTAAGATCAAAGGAAGCCTGAA	1914
QY	1861	GTGGAGAAATATCGGAAACTGGAGAAGATCAATGCTGAGCAGCAGCTCAAAATTCAGAG	1920
Db	1915	GTGGAGAAATATCGGAAACTGGAGAAGATCAATGCTGAGCAGCAGCTCAAAATTCAGAG	1974
QY	1921	CTCCAAAGGAATCTGGAGAGGCTG-----	1945
Db	1975	CTCCAAAGGAATCTGGAGAGGCTGTAAGAACCAAGACCGAAGCCACCGAGCTGTCAG	2034
QY	1946	-----CAAGAGAGCGAAGCGGAGAGGAGCTGAGAGAAGCTGAGAACCGAGACCGAG	1992
Db	2035	AATATCCGCCACAGGCAAAAGAGCGAGCGGAGAGGAGCTGAGAGAAGCTGAGAACCGAGAG	2094
QY	1993	GATTCCTTCTGAAGGATCAAGAAAGACTGTGTGAAGCTGAGGAAAGCGCCGCAATTCCTG	2052
Db	2095	GATTCCTTCTGAAGGATCAAGAAAGACTGTGTGAAGCTGAGGAAAGCGCCGCAATTCCTG	2154
QY	2053	GAGAAACAAGGTAAAGAGACTAGAGACATGAGAGGCTGTGAAGAAACAAGTAAGAGATGAC	2112
Db	2155	GAGAAACAAGGTAAAGAGACTAGAGACATGAGAGGCTGTGAAGAAACAAGTAAGAGATGAC	2214
QY	2113	ATCCAGCAAAATCCCAACAGATTCAGACAGATGGCTGTAAATTTCTGAGACTCGAAGAG	2172

Db	2215	ATCCAGACAAATATCCACAGATCCAGATGGCGTGAATTAATTTGAGACTCCAGAG	227
Qy	2173	AAACATTCGGGAGGCCCAAGTCTTCAGCCGACACTTGAAGTGCACCTGAAACAGAAAG	223
Db	2275	AAACATTCGGGAGGCCCAAGTCTTCAGCCGACACTTGAAGTGCACCTGAAACAGAAAG	223
Qy	2233	CAGCACTATGAGGAAAAGTTAAAGTGTGGAACAATCAGATTAAGAAAGACCTGGCTGAC	229
Db	2335	CAGCACTATGAGGAAAAGTTAAAGTGTGGAACAATCAGATTAAGAAAGACCTGGCTGAC	239
Qy	2293	AAGGAGACACTGGAGAACATGATGCAGAGACACGAGAGAGAGCCCATGAGAGGCCAAA	235
Db	2395	AAGGAGACACTGGAGAACATGATGCAGAGACACGAGAGAGAGCCCATGAGAGGCCAAA	245
Qy	2353	ATTCTCAGGGAACAGAAAGCGATGATCAATGCTATGAGATCCAAATCAGATCCCTGGAA	241
Db	2455	ATTCTCAGGGAACAGAAAGCGATGATCAATGCTATGAGATCCAAATCAGATCCCTGGAA	251
Qy	2413	CAGAGGATTTGGAACTGTCTGAAGCCATAAATTGACACAAATAGCAGTCTTTTAC	247
Db	2515	CAGAGGATTTGGAACTGTCTGAAGCCATAAATTGACACAAATAGCAGTCTTTTAC	257
Qy	2473	CAAAAGGACATGAAGGCCCAAGAAAGATGATTTCTGAATCTCAGGCAACAGAAATTTAC	253
Db	2575	CAAAAGGACATGAAGGCCCAAGAAAGATGATTTCTGAATCTCAGGCAACAGAAATTTAC	263
Qy	2533	CTGGAGACACAGGCTTGGAAATTGAGGCCCAAGAACCGAAACTGGAAGAGCAGCTGGAG	259
Db	2635	CTGGAGACACAGGCTTGGAAATTGAGGCCCAAGAACCGAAACTGGAAGAGCAGCTGGAG	269
Qy	2593	AAGATCAAGCCACCAAGAACCAAGTGAACAAGATTCGGCTGCTGGAATCTGGAACAAGATTG	265
Db	2695	AAGATCAAGCCACCAAGAACCAAGTGAACAAGATTCGGCTGCTGGAATCTGGAACAAGATTG	275
Qy	2653	CGGAGAGTCAAGTCTAGAGCACAGGAGCAGAACTGAGACTCAAGCCGACACTCAGAG	271
Db	2755	CGGAGAGTCAAGTCTAGAGCACAGGAGCAGAACTGAGACTCAAGCCGACACTCAGAG	281
Qy	2713	CTACAGCTCTCCCTGACAGAGCGCGAGTCAAGTTGAGAGCCCTGCGAGGCTGCACGGCG	277
Db	2815	CTACAGCTCTCCCTGACAGAGCGCGAGTCAAGTTGAGAGCCCTGCGAGGCTGCACGGCG	287
Qy	2773	GCCCTGAGAGCGCAGCTTCGCGACGCGAAGACAGAGCTGGAAGAGACCAACGACGAAGCT	283
Db	2875	GCCCTGAGAGCGCAGCTTCGCGACGCGAAGACAGAGCTGGAAGAGACCAACGACGAAGCT	293
Qy	2833	GAAAGGAGATTCAGGCACTACCGGCACATGAGATGAATTCAGCGCAATTTGATGCT	289
Db	2935	GAAAGGAGATTCAGGCACTACCGGCACATGAGATGAATTCAGCGCAATTTGATGCT	299
Qy	2893	CTTCTGTAACAGCTGATCTGTAATCAGACAGACTCGGAGGAGCGCTAAACAGCTGACCGAG	295
Db	2995	CTTCTGTAACAGCTGATCTGTAATCAGACAGACTCGGAGGAGCGCTAAACAGCTGACCGAG	305
Qy	2953	GACAAAGCTGAACTTCACAAACCAAACTTCTACTTGTCCAAACAACTCGATGAGGCTTCT	301
Db	3055	GACAAAGCTGAACTTCACAAACCAAACTTCTACTTGTCCAAACAACTCGATGAGGCTTCT	311
Qy	3013	GGCGCGAACGAGGATTTGTACAACTCGCGAAGTGAAGTGAACCATTCGCCCGGGAATC	307
Db	3115	GGCGCGAACGAGGATTTGTACAACTCGCGAAGTGAAGTGAACCATTCGCCCGGGAATC	317
Qy	3073	ACGGAACGAGAGATGACAGCTTACCAGCCAGAAAGCAACGATGAGGCTCTGAAACCAAG	313
Db	3175	ACGGAACGAGAGATGACAGCTTACCAGCCAGAAAGCAACGATGAGGCTCTGAAACCAAG	323
Qy	3133	TGCACAAATGCTGAGAGGAACAGGTATGAGATTTGGAAGCCCTTAAACATGAGCTGTAAGAA	319
Db	3235	TGCACAAATGCTGAGAGGAACAGGTATGAGATTTGGAAGCCCTTAAACATGAGCTGTAAGAA	329
Qy	3193	AAAAGCGCGCAGTGGAGGCGCTGGAGAGCGCTCGGGGTATAGAAATCCCAATTGGAG	325

Db	3295	AAAGAGCGGCAATGCGGAGGCGCTCGAGGAGCGCTCTGGGTGATGAGAAATCCAGTTT9AG	3354
Oy	3253	TGTGCGGGTTCGAGAGCTGCAAGAAATGCTTGGACACCGAGAAACAGAGCGCGAGAGCC	3312
Db	3355	TGTCGGGTTCGAGAGCTGCAAGGATGCTGGACACCGAGAAACAGAGCGCGAGAGCC	3414
Oy	3313	GATCAGCGGGATCAACGAGCTCTCCGAGGTGGTGGAGCTGGGAGTGAAGAACACAAAGGCT	3372
Db	3415	GATCAGCGGGATCAACGAGCTCTCCGAGGTGGTGGAGCTGGGAGTGAAGAACACAAAGGCT	3474
Oy	3373	GAGATTCTCGCTCTGCAAGGCTCTCAAGAGCGAAGCTGAAGGCGGAGAGCTCTCT	3432
Db	3475	GAGATTCTCGCTCTGCAAGGCTCTCAAGAGCGAAGCTGAAGGCGGAGAGCTCTCT	3534
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; APPLICANT: Fridlie, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1e1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
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RESULT 8
US-10-791-666-1
; Sequence 1, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; PRIOR FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335

PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens
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Query Match 91.9%; Score 5661.4; DB 18; Length 6165;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 16; Indels 243; Gaps 3;
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Db 2881 GAAAGAGAGATCCAGAGCACTCAGGCAATGAGAGATGAATTCAGGCGCAATTTGATGCT 2940
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|
|
QY 2893 CTTCTGTAACAGCTGTACTGTAACTACAGAGCTGGAAGAGAGAGCTTAAACCAAGCTGACCGAG 2952
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|
Db 2941 CTTCTGTAACAGCTGTACTGTAACTACAGAGCTGGAAGAGAGAGCTTAAACCAAGCTGACCGAG 3000
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|
QY 2953 GACAAGCTGAACTCAACCAAACTTCTACTTGTCCAAACAATCTGATGAGGCTTCT 3012
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|
Db 3001 GACAAGCTGAACTCAACCAAACTTCTACTTGTCCAAACAATCTGATGAGGCTTCT 3060
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|
|
QY 3013 GCGGCCAAGAGAGATTTGTAACAATGCGAAGTGAAGTGAACATCTCCGCGGAGAGATC 3072
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Db 3061 GGGCCAAAGACGATTGTCAACTGCGAAGTGAATGAGACATCTCGCGGAGATC 3120
QY 3073 ACGGAACGAGAGATGCAAGCTTACCAGCCAGAACCAATGAGAGCTCTGAAGACGAG 3132
Db 3121 ACGGAACGAGAGATGCAAGCTTACCAGCCAGAACCAATGAGAGCTCTGAAGACGAG 3180
QY 3133 TGCACATCTGAGAGAACAGGTCTATGATTTTGAAGGCTCTAAACGATGAGCTAGAA 3192
Db 3181 TGCACATCTGAGAGAACAGGTCTATGATTTTGAAGGCTCTAAACGATGAGCTAGAA 3240
QY 3193 AAAGACGAGCAGTGGAGGCTTGAAGAGGCTCTGAGTATGAGAAATCCAGTTTGA 3252
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QY 3253 TGTGCGGTTTGAAGAGCTGCAAGAAATGCTGGAACAAGAAACAGAGCGAGAGACC 3312
Db 3301 TGTGCGGTTTGAAGAGCTGCAAGAAATGCTGGAACAAGAAACAGAGCGAGAGACC 3360
QY 3313 GATCAGCGGATCAACGAGTCTGCGCAGGTGTGAGCTGAGTGAAGGAGCAAGAGCT 3372
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QY 3373 GAGATTCTGCTCTGAGAGAGGCTCTCAAGACAGAGCTGAAGGCGAGAGCTCTCT 3432
Db 3421 GAGATTCTGCTCTGAGAGAGGCTCTCAAGACAGAGCTGAAGGCGAGAGCTCTCT 3480
QY 3433 GACAGCTCAATGACTCTGGAAGAAAGCATGCTATGCTTGAATGAAATGCCAGACTTA 3492
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Db 3541 CAGCAAGCTGAGACTGAAGAGAGCTCAACAGAGCTTGTGAAGAGCAAGGCAAA 3600
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Db 3601 TTACAGCAGCAGATGAGACTGACGAAATAATCATTTTCGTCGTCGACGAGCTGCA 3660
QY 3613 GAAAGCTTGAATGAGAGCTGATCTATGAAAGCAAGAAAGATGACTTGAAGTACGCTG 3672
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Db 3721 GAAAAATTCAGGTTCTATCTCATGAAAGGTAAAAATGGAAGGCACTATTTCTCA 3780
QY 3733 CAACCAAACTCATTTATTTTCTGCAAGCCAAATGAGCAACCTCTAAAAAGAAAG 3792
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QY 3793 GGTATTATTAGTGAAGGAAAGAGACCTGCTTTAACCAACAGGTTCTCTGAGTAC 3852
Db 3839 -----AGGTTCTCTGAGTAC 3855
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Db 3856 AATGAGCTGAAGCTGGCCCTGAGAGAGAAAGCTCGCTGACAGCTAAGAGAGCC 3915
QY 3913 CTTTCAAGAAACCGCATGAGCTCCGGTCCGCCGAGAGAAAGCTCCCAACGCAAGCA 3972
Db 3916 CTTTCAAGAAACCGCATGAGCTCCGGTCCGCCGAGAGAAAGCTCCCAACGCAAGCA 3975
QY 3973 ACGGACCAACCAACCATTCACGCGAGCCACCGGAGGAGAGATGTCATGTCGCGC 4032
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QY 4033 ATCTGCGGTTTGGCAAGAGCAAGCCCATGTCATAGAGCTGTGGCCCGGCAATCAGC 4092
Db 4036 ATCTGCGGTTTGGCAAGAGCAAGCCCATGTCATAGAGCTGTGGCCCGGCAATCAGC 4095
QY 4093 CCGCAAGAAAGAGTCTTCAACTCGAAGAGAAATTTAGTGGCGTCTTAAGAAACGATGAC 4152
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QY 4153 CACAAATTTCTCAACCGATTTCACGTAAGACTGAACATGCGAGCCCAAAAGTGTCTG 4212
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QY 4213 TGTCTGATACCGTGCATCTTGAAGCGCCAGCATCAATGTCTGAAATGTGAGTATG 4272
Db 4216 TGTCTGATACCGTGCATCTTGAAGCGCCAGCATCAATGTCTGAAATGTGAGTATG 4275
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QY 4453 GGAACGAAAGGCTGGAGACAGAAATGATTTGCTGAGAGGATCAAAAGTCTCATTTAT 4512
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QY 4573 GACGGGAGATGTATCTATTATCATGATGCGGTGTGCTTCCGAATCTGCAAAATACAGCAAA 4632
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QY 4633 GCA----- 4635
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Db 4756 GAATCAGTTGTGCAAGGTGGAGAGTTTCTAGGAGAAAGCAAGAGCTGATCTAACTG 4815
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Db 4816 CTTGGAATCTCCCTGCTGAACTGGAAGGTATGACGCTTGAACATGACGAGCTG 4875
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Db 5056 GTGAAGAAAGTGAACAGTCCCTGCGCCAGTCCCACTGTGCTGCCAGCCGACATTCGA 5115
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Db 5116 CCGCAATTTTGAAGTGTCAAGGAGCTGCCACTTGTGTGGGGGAGGGAAGTTAGAAC 5175
QY 5023 GGGCTCTGATCTGTGACAGCATGCGCAGCAAAAGTGTCAATTTCTCGCTACAAACGAAAC 5082
Db 5176 GGGCTCTGATCTGTGACAGCATGCGCAGCAAAAGTGTCAATTTCTCGCTACAAACGAAAC 5235

OY	5083	TTCCAGCAATCTCGATATCCGAAAGAGATAGACCTTCAGAGCCCTGAGCGCTGATCCAC	5142
Db	5236	CTCGCAATATCTGATCCGGAAGAAGATAGACCTTCAGAGCCCTGAGCGCTGATCCAC	5295
OY	5143	TTCAACCAATTACAGTATCTCATTTGGAACCAATAAATTTCAACGAATGACATGAAGACG	5202
Db	5296	TTCAACCAATTACAGTATCTCATTTGGAACCAATAAATTTCAACGAATGACATGAAGACG	5355
OY	5203	TACACGCTCGAGGAATTTCTGGATTAAGATGACATTTCTTTGGACCTGCTGTGTTGGC	5262
Db	5356	TACACGCTCGAGGAATTTCTGGATTAAGATGACATTTCTTTGGACCTGCTGTGTTGGC	5415
OY	5263	GCCCTTCACACAGCTTCCCTGTCATATCGAGCGAGTGAACAGCGACGGGACGCGAG	5322
Db	5416	GCCCTTCACACAGCTTCCCTGTCATATCGAGCGAGTGAACAGCGACGGGACGCGAG	5475
OY	5323	GAGTACTTGCTGTGTGTTTCCAGAAATTTTGGAGTGTCGTGCAATTTCTTACGGAAGACGTAGC	5382
Db	5476	GAGTACTTGCTGTGTGTTTCCAGAAATTTTGGAGTGTCGTGCAATTTCTTACGGAAGACGTAGC	5535
OY	5393	CGCACAGACGATCTTCAGTGAATGCGCTTACCTTTGGCCTTTGCCCTTACAGAAACCTTAT	5442
Db	5536	CGCACAGACGATCTTCAGTGAATGCGCTTACCTTTGGCCTTTGCCCTTACAGAAACCTTAT	5595
OY	5443	CTGTTTGTGACCCACATTTCAACATCACTCGAAGTAATTGAGATCCAGGGACGGCTCCACACA	5502
Db	5596	CTGTTTGTGACCCACATTTCAACATCACTCGAAGTAATTGAGATCCAGGGACGGCTCCACACA	5655
OY	5503	GGGACCCCTGCGCCGACGCTACCTGAGCAATCCGGAACCCGCGCTACCTGGGCGCTGCAATT	5562
Db	5656	GGGACCCCTGCGCCGACGCTACCTGAGCAATCCGGAACCCGCGCTACCTGGGCGCTGCAATT	5715
OY	5563	TCTCTCAGAGACGATTTTACTTGGCGTCTCTCATACAGGATTAATTTAAGGTCATTTTGTGCG	5622
Db	5716	TCTCTCAGAGACGATTTTACTTGGCGTCTCTCATACAGGATTAATTTAAGGTCATTTTGTGCG	5775
OY	5623	AAGGGAACCTCGTGAAGAAGTCGCGGACCTGAACACCAACCGGGGCGCGTCCACCTCCGCG	5682
Db	5776	AAGGGAACCTCGTGAAGAAGTCGCGGACCTGAACACCAACCGGGGCGCGTCCACCTCCGCG	5835
OY	5683	AGCAACCCCAACAAACGAGGCCCAACCCACGTACAACGAGCAATCAACCAAGGCGCTGGCC	5742
Db	5836	AGCAACCCCAACAAACGAGGCCCAACCCACGTACAACGAGCAATCAACCAAGGCGCTGGCC	5896
OY	5743	TTCACCCCAAGCGCGCGCCGAGAGGCCCAACCCGCGAGAGCCAAACACCCCAACCGC	5802
Db	5896	TTCACCCCAAGCGCGCGCCGAGAGGCCCAACCCGCGAGAGCCAAACACCCCAACCGC	5955
OY	5803	TACCCCGAGGGGCGGACCGAGCTGCGGACGGGACAGATGTCCTGGGCGGCGCCCTGGAGCGA	5866
Db	5956	TACCCCGAGGGGCGGACCGAGCTGCGGACGGGACAGATGTCCTGGGCGGCGCCCTGGAGCGA	6015
OY	5863	GAGAAATCCCCCGCGCGCGATGCTCAGACACGCGAGAGAGACGCTGCCCGGAGAGCGTGT	5922
Db	6016	GAGAAATCCCCCGCGCGCGATGCTCAGACACGCGAGAGAGACGCTGCCCGGAGAGAGCGTGT	6075
OY	5923	GAAGACAGAGCAAGGGGCGGCTGCTGCGGAGCCGTGAGGACCCCGCTGTCCAGGTTG	5988
Db	6076	GAAGACAGAGCAAGGGGCGGCTGCTGCGGAGCCGTGAGGACCCCGCTGTCCAGGTTG	6135
OY	5983	AACAGAGGAAGAGGCGAGAGTGC	6005
Db	6136	AACAGAGTCTGGGACCAAGTCTTC	6158

DB	Seq ID	Sequence	Score	DB	Length	Matches	Mismatches	Indels	Gaps
DB	1	ATGTTGAAGTTCAAATATATAGAGCCGCGAATCTTTGATGCTGCTGCTGCAACCCATT	91.8%	DB 18	8656	37	246		4
DB	51	ATGTTGAAGTTCAAATATATAGAGCCGCGAATCTTTGATGCTGCTGCTGCAACCCATT	95.5%	DB 18	8656	37	246		4
DB	61	GCCAGCCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTATGACTCA	95.5%	DB 18	8656	37	246		4
DB	111	GCCAGCCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTATGACTCA	95.5%	DB 18	8656	37	246		4
DB	121	CAGAGATGTCCTCTCTTCCCGAAGAGATATTAGATGCTCTCTTCTCTTTGAA	95.5%	DB 18	8656	37	246		4
DB	171	CAGAGATGTCCTCTCTTCCCGAAGAGATATTAGATGCTCTCTCTCTTTGAA	95.5%	DB 18	8656	37	246		4
DB	181	GAATGCAATGACCTGCTCTGATGAAATTAAGCACTGAGCAATTTGTCGGGAA	95.5%	DB 18	8656	37	246		4
DB	231	GAATGCAATGACCTGCTCTGATGAAATTAAGCACTGAGCAATTTGTCGGGAA	95.5%	DB 18	8656	37	246		4
DB	238	TATTCGCAACCATATAGCTGATTAAGAGCTCCAGCTTGGCGAAGGACTTTCGAGTC	95.5%	DB 18	8656	37	246		4
DB	291	TATTCGCAACCATATAGCTGATTAAGAGCTCCAGCTTGGCGAAGGACTTTCGAGTC	95.5%	DB 18	8656	37	246		4
DB	298	AGAGCTCTTGAAGTGTGCTCACTTGTCTGAATGCTGAGGTGTAAGAGAAACCAAC	95.5%	DB 18	8656	37	246		4
DB	351	AGAGCTCTTGAAGTGTGCTCACTTGTCTGAATGCTGAGGTGTAAGAGAAACCAAC	95.5%	DB 18	8656	37	246		4
DB	358	GGGAGCATATATGCTATGAAAGTGAAGAAAGGCTTATATGAGGAGAGAGGTT	95.5%	DB 18	8656	37	246		4
DB	411	GGGAGCATATATGCTATGAAAGTGAAGAAAGGCTTATATGAGGAGAGAGGTT	95.5%	DB 18	8656	37	246		4
DB	418	TCATTTTGAAGAAAGCGGAAATATATCTCGAAGCAACGCCCTGTGATCCGCCAA	95.5%	DB 18	8656	37	246		4
DB	471	TCATTTTGAAGAAAGCGGAAATATATCTCGAAGCAACGCCCTGTGATCCGCCAA	95.5%	DB 18	8656	37	246		4
DB	478	TTACGATATGCTTTACAGAAACCAATACCTTATCTGATGGAATATATAGCTGGA	95.5%	DB 18	8656	37	246		4
DB	531	TTACGATATGCTTTACAGAAACCAATACCTTATCTGATGGAATATATAGCTGGA	95.5%	DB 18	8656	37	246		4
DB	538	GGGAGCTGCTGCTCACTTTGATATGATGAGCAAGTTAGATGAAACCTGATACAG	95.5%	DB 18	8656	37	246		4
DB	551	GGGAGCTGCTGCTCACTTTGATATGATGAGCAAGTTAGATGAAACCTGATACAG	95.5%	DB 18	8656	37	246		4
DB	558	TTTATCTGATGCTGCTGATTTTGGCTGTTCAAGCGTTCACTGATGGAATATAGCTGAT	95.5%	DB 18	8656	37	246		4
DB	651	TTTATCTGATGCTGCTGATTTTGGCTGTTCAAGCGTTCACTGATGGAATATAGCTGAT	95.5%	DB 18	8656	37	246		4
DB	658	CGAGACATCAAGCTGAGAACTTCCTGTTGACCGCAAGCAATCAAGCTGATGAT	95.5%	DB 18	8656	37	246		4
DB	711	CGAGACATCAAGCTGAGAACTTCCTGTTGACCGCAAGCAATCAAGCTGATGAT	95.5%	DB 18	8656	37	246		4
DB	718	TTTGATCTGCGCGAAGAAATGATTAACAAGATGATGATGCAACTCCGATGGA	95.5%	DB 18	8656	37	246		4
DB	771	TTTGATCTGCGCGAAGAAATGATTAACAAGATGATGATGCAACTCCGATGGA	95.5%	DB 18	8656	37	246		4
DB	778	ACCCAGATTAATGCTCTGAAATGCTGATGAAAGAGGAGATGAAAGGCAAC	95.5%	DB 18	8656	37	246		4
DB	831	ACCCAGATTAATGCTCTGAAATGCTGATGAAAGAGGAGATGAAAGGCAAC	95.5%	DB 18	8656	37	246		4

838 TACGGCTGGACATGATCTGTGTGTCAGTGGCGGTGATTTGCCATGATGATTTATGGG 897
891 TACGGCTGGACATGATCTGTGTGTCAGTGGCGGTGATTTGCCATGATGATTTATGGG 950
898 AGATCCCCCTTGCAGAGGGAACTCTGCAGAACCTTCAATTAATTAATTTCCAG 957
951 AGATCCCCCTTGCAGAGGGAACTCTGCAGAACCTTCAATTAATTAATTTCCAG 1010
958 CCGTTTTTGAATTTTCAGATGACCCCAAGTGAGAGATCTTTCTTGAATCTGATTCAA 1017
1011 CCGTTTTTGAATTTTCAGATGACCCCAAGTGAGAGATCTTTCTTGAATCTGATTCAA 1070
1018 AGCTTTGTGTGGCCCAAGAAAGAGATGAACTTTGAAAGTCTTTGCTGCCATCTCTTC 1077
1071 AGCTTTGTGTGGCCCAAGAAAGAGATGAACTTTGAAAGTCTTTGCTGCCATCTCTTC 1130
1078 TTCTCTAAATTTGATCTGGAACAACATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1137
1131 TTCTCTAAATTTGATCTGGAACAACATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1190
1138 AAGTCTGACGATGACATCTTCAATTTTGTATGAAACAGAGAAATTCGTGGTTTCATCC 1197
1191 AAGTCTGACGATGACATCTTCAATTTTGTATGAAACAGAGAAATTCGTGGTTTCATCC 1250
1198 TCTCCGTGCGAGTGAAGCCCTCAGGCTTCTCGGGTGAAAGAACTGGCCGTTTGGGGTTT 1257
1251 TCTCCGTGCGAGTGAAGCCCTCAGGCTTCTCGGGTGAAAGAACTGGCCGTTTGGGGTTT 1310
1258 TCGTACAGCAAGGCACTGGGGATTTCTTGTGATCTGAGCTGTGTGTCTGGGCTGAGC 1317
1311 TCGTACAGCAAGGCACTGGGGATTTCTTGTGATCTGAGCTGTGTGTCTGGGCTGAGC 1370
1318 TCCCTCTGCAAGACTAGCTTCATGAGAAAGAACTTCTCATCAAAAGCAAGGCTACAA 1377
1371 TCGCCCTCCAGACTAGCTTCATGAGAAAGAACTTCTCATCAAAAGCAAGGCTACAA 1430
1378 GACTCTCAGAGCAAGTGTCACAAGATGAGCAGAGAAATGACCCGGTTACATCGGAGAGTG 1437
1431 GACTCTCAGAGCAAGTGTCACAAGATGAGCAGAGAAATGACCCGGTTACATCGGAGAGTG 1490
1438 TCGAGAGTGGAGCTGTGCTAGTCAAGAGAGTGGAGCTGAGAGGCTCTGAGACTCAG 1497
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1498 AGATCCCTCTGAGAGAGACCTTGTCTACCTACATCAAGAAATGACAGTAAAGCGA 1557
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1558 AGTTTGGAGCAAGCAGATGAGAGTGTCCAGAGAGATGACAAAGCATGACGCTTCTC 1617
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1618 CATGATATCAGAGAGAGAGCCGGAAGCTTCAAGAAATCAAGAGAGAGAGTCCAGGCT 1677
1671 CATGATATCAGAGAGAGAGCCGGAAGCTTCAAGAAATCAAGAGAGAGAGTCCAGGCT 1730
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1918 GAGCTCCAAAGAGAACTGAGAGGCT----- 1944
1971 GAGCTCCAAAGAGAACTGAGAGAGGCTTTAAAGCCAGACCGAGGCTCAGGAGCTGCTG 2030
1945 -----GCAAAGAGCGAGCCGAGAGGAGCTGAGAGAGCTGAGAAACCGA 1989
2031 CAGAAATATCCGCGAGCAAGAGAGCGAGCCGAGAGGAGCTGAGAGAGCTGAGAAACCGA 2090
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2091 GAGGATTTCTTGAAGGCTTCAGAAAGAAAGCTGTGTGAAGCTGTGAGAAAGCTCCCTTCT 2150
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2991 GCTCTTCTGTAACAGCTGTAATCTGTAATCAAGACCTGAGAGAGCAGCTAAACAGCTGAGC 3050
2950 GAGGACAAACGCTGAATCAACAAACAACTTCACTTGTCCAAACAACTGATGAGGCT 3009

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RESULT 10
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 ; GENERAL INFORMATION:
 ; APPLICANT: Gerlach, Valerie L
 ; APPLICANT: MacDougall, John R
 ; APPLICANT: Smithson, Glenda
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 ; APPLICANT: Stone, David
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Grose, William M
 ; APPLICANT: Alsebrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Spyrek, Kimberly A
 ; APPLICANT: Leach, Martin D
 ; APPLICANT: Shinkets, Richard A
 ; TITLE OF INVENTION: No. US20040043926A1e1 Proteins and Nucleic Acids Encoding Same
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 ; PRIOR APPLICATION NUMBER: 60/276,667
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/294,823
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 ; PRIOR APPLICATION NUMBER: 60/304,868
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 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: PatentIn Ver. 2.1
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 ; LENGTH: 6189
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-964-956-10
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Db 3718 GAAAAATTGAGGTTCTTATCTCATGAAAAGTGAAATGAAAGGCACTATTTCTCA 3777
Qy 3733 CAAACCAATCTATGATTTTCTGCAAGCCAAATGAGCAACTGCTTAAGAAAGAAAG 3792
Db 3778 CAAACCAATCTATGATTTTCTGCAAGCCAAATGAGCAACTGCTTAAGAAAGAAAG -- 3835
Qy 3793 GGTATTATTAATGACAGGAAAGAGACCTGCTTAAACCAACAGAGTTCTCTGAGTAC 3852
Db 3836 -----AGTGCTCTGACGATAC 3852
Qy 3853 AATGACTGAGACTGAGCCCTGAGAAAGAAAGTCTGCTGTCAGAGCTGAAGAGCC 3912
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Qy 3913 CTTCAAGAAAGCCGATGAGCTCCGCTCCGCGGAGAGAGCTGCCAAGCAAGAA 3972
Db 3913 CTTCAAGAAAGCCGATGAGCTCCGCTCCGCGGAGAGAGCTGCCAAGCAAGAA 3972
Qy 3973 ACGGACCAACGACCAACCATCAAGCCAGGCAAGGAGAGAGCTGCAATGCTGCGC 4032
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Qy 4033 ATCTGCGGTGCGCAGAGACCAAGCCAGTGCATGAGCTTGCGCCCGCATCAGC 4092
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Qy 4093 CCGAGAAAGAGTCTTCAACTCAGAGAAATTTAGTCCGCTTTAAGAAAGCATGAC 4152
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Qy 4153 CACAATATTCTCAACGATTTCAACGTAAGGAGTGAACATGAGAGCAAAAGTGTCTGTG 4212
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Qy 4213 TGTCTGATACCGTGAACCTTGAAGCCAGGAGTCCAAATGTCAGAAATGTCAGGTGATG 4272
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Qy 4273 TGTCAACCCCAATGCTCCAGCTGCTTGCAGGCACTGCGGCTTGCCTGTAATGTGC 4332
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Db 4333 ACACACTTCAACGAGGCTTCTGCGGTGACAAATGAACTCCCAAGTCTCAGACCAAG 4392
Qy 4393 GAGCCAGAGAGCTTGAACCTGAAAGGAGTGAAGTGCACAGAAATTAACAAAGCA 4452
Db 4393 GAGCCAGAGAGCTTGAACCTGAAAGGAGTGAAGTGCACAGAAATTAACAAAGCA 4452

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4455 GGAACAGCAAGCTGGGACAGAAATGATCTTGTCTTGGAGGATCAAAAGTCCATTTAT 4512
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4513 GACAAATGAAGCCAGAGAACTGGACAGAGCCGCTGGAAGAAATTTGAGCTGTCTCC 4572
4573 GACGGGAGATGATATCTATGATGTCGCTTGGCTTCCGAACTCGCAATTAAGCCAA 4632
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4813 CTGGGAACTCCCTGCTGAAACTGGAGAGTGAACCGTCTAGACATGAACTGACAGCTG 4872
4723 CCCTTCAGTGACCAAGGTGTGTGTGTGGGACCGAGAGAGGGCTCTACGCTCTGATGTC 4782
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4783 TTGAAAACTCCCTTAACCATGATCCAGGAAATTTGAGCACTCTTCAATTAATTAATC 4842
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4843 AAGACCTGAGAGACTACTCATGATAGCAGAGAGAGAGGAGGACTGTGTCTTGTGAC 4902
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5293 TTACCAATTTACGATCTCTCATTTGAAACCAATTAATTTCAAGAAATGACATGAAGAG 5352
5203 TACACGCTGAGGAATTCCTGATTAAGATGACATTCCTTGGGACCTGTGTGTTC 5262
5353 TACACGCTGAGGAATTCCTGATTAAGATGACATTCCTTGGGACCTGTGTGTTC 5412
5263 GCTCTTTCACAGCTTCCCTGTCTCAATCTGTGACAGTGAACAGGAGGAGGAGAGAG 5322
5413 GCTCTTTCACAGCTTCCCTGTCTCAATCTGTGACAGTGAACAGGAGGAGGAGAGAG 5472
5323 GAGTACTGTGTGTTCACAGAAATTTGAGAGTGTGAGAGTCTTAAGGAAAGAGTGGC 5382
5473 GAGTACTGTGTGTTCACAGAAATTTGAGAGTGTGAGAGTCTTAAGGAAAGAGTGGC 5532

QY 5383 CGCAGAGAGATCTCAAGTGAAGTGCCTTACCTTTGAGCTTTGAGAGAGAGAGCCAT 5442
Db 5533 CGCAGAGAGATCTCAAGTGAAGTGCCTTACCTTTGAGCTTTGAGAGAGAGAGCCAT 5592
QY 5443 CTGTTGTGACCCCACTTCACTCACTGAAATTAATTAAGATCAGAGCAAGCTCTCAGCA 5502
Db 5593 CTGTTGTGACCCCACTTCACTCACTGAAATTAATTAAGATCAGAGCAAGCTCTCAGCA 5652
QY 5503 GGGAGCCCTGAGGAGCTTACTGAGCAATCCGAAACCCGCGTACTGAGGAGCCCTGCAAT 5562
Db 5653 GGGAGCCCTGAGGAGCTTACTGAGCAATCCGAAACCCGCGTACTGAGGAGCCCTGCAAT 5712
QY 5563 TCCTCAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5622
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Db 5773 AAGGAAACCTGTGAAAGAGTCCGAGCACTGAACCAACCGGAGCCGCTTCACTCCGC 5832
QY 5683 AGCAGCCCAACAGAGAGGAGCCACCCAGTACCAACAGAGCAATACCAAGAGGAGGAGCC 5742
Db 5833 AGCAGCCCAACAGAGAGGAGCCACCCAGTACCAACAGAGCAATACCAAGAGGAGGAGCC 5892
QY 5743 TCAGAGCCAGAGGAGCCAGAGAGCCAGAGAGCCAGAGAGCCAGAGAGCCAGAGAGCC 5802
Db 5893 TCAGAGCCAGAGGAGCCAGAGAGCCAGAGAGCCAGAGAGCCAGAGAGCCAGAGAGCC 5952
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Db 5953 TACCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6012
QY 5863 GAGAGATCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5922
Db 6013 GAGAGATCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6072
QY 5923 GAAGACAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5982
Db 6073 GAAGACAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6132
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Db 6133 AACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6187

RESULT 11
US-10-262-511-1
; Sequence 1, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Miller, Isabelle
; APPLICANT: Feyman, John A.
; APPLICANT: Kekuda, Rameah
; APPLICANT: Ju, Jinfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Paturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Carterton, Blina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.

APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkete, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuroSeqList version 0.1
SEQ ID NO 1
LENGTH: 6189
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(6159)
US-10-262-511-1

Query Match 91.4%; Score 5631; DB 17; Length 6189;
Best Local Similarity 95.3%; Pired. No. 0;
Matches 5944; Conservative 0; Mismatches 45; Indels 246; Gaps 4;

QY 1 ATGTTGAAGTTCAATATGAGAGCGCGAAATCCTTGGATGCTGTGCTGAACCAT 60
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QY 61 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCAGAGGGAACACCCCTTTATGACTCA 120
DB 61 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCAGAGGGAACACCCCTTTATGACTCA 120
QY 121 CAGCAGATGCTCTCTCTTCCGAGAAAGGATATTAGTACCCTTTGTTCTCTTTGAA 180
DB 121 CAGCAGATGCTCTCTCTTCCGAGAAAGGATATTAGTACCCTTTGTTCTCTTTGAA 180
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DB 181 GAATGAGTCAGGCTGCTGATGAGATTAAAGCAGTGAGCAACTTTGTCGGAGATAT 240
QY 241 TCCGACACCATAGCTAGTTTACAGAGCTTCAGCCTTCGCAAAAGGACTTCGAAATCAG 300
DB 241 TCCGACACCATAGCTAGTTTACAGAGCTTCAGCCTTCGCAAAAGGACTTCGAAATCAG 300
QY 301 AGCTCTGTAGTGTGTGTCTCTTCTGTAAGTCAAGTGTATAGAGAGAAAGCAACCGG 360
DB 301 AGCTCTGTAGTGTGTGTCTCTTCTGTAAGTCAAGTGTATAGAGAGAAAGCAACCGG 360
QY 361 GACATCTATGCTTAAAGTATGAGAGAAAGGCTTTATTTGGCCAGAGAGAGTTTCA 420
DB 361 GACATCTATGCTTAAAGTATGAGAGAAAGGCTTTATTTGGCCAGAGAGAGTTTCA 420

QY 421 TTTTGAAGAGAGCGGAACAATATTATCTGAAGCAAGCCCGTGGATCCCAATTA 480
DB 421 TTTTGAAGAGAGCGGAACAATATTATCTGAAGCAAGCCCGTGGATCCCAATTA 480
QY 481 CAGTATGCTTTCAGGACAAATAATCACTTTATCTGATGAGAGAAATATCAGCTGAGG 540
DB 481 CAGTATGCTTTCAGGACAAATAATCACTTTATCTGATGAGAGAAATATCAGCTGAGG 540
QY 541 GACTGTCTGTCACTTTGATATGATGAGAACCACTTATGATGAAACCTGATACGTTT 600
DB 541 GACTGTCTGTCACTTTGATATGATGAGAACCACTTATGATGATGAAACCTGATACGTTT 600
QY 601 TACCTAGCTGACTGATTTTGGCTGTTCACAGCTTCACTGATGAGATACGTCATCA 660
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DB 661 GACATCAAGCTGAGAACATTCCTGTTAGCCGACAGACATCAAGCTGTGATTTT 720
QY 721 GGAATCGCGGAAATGAATCAACAGATGTGATGCCAACTCCGATGGGACC 780
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QY 778 CAGATTAATAGGCTCTGTAAGTGTGATGATGAGAGGGGATGAGAAAGGACACTAC 840
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QY 841 GGCTTGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
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QY 961 TTTTGAATTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
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DB 1321 CCGTCCAGCTGAGCCCTCAGGCTTCTGCGGTGAAGAACTGCGGTTTGAGGATTTTGG 1380
QY 1318 CCGTCCAGCTGAGCCCTCAGGCTTCTGCGGTGAAGAACTGCGGTTTGAGGATTTTGG 1377
DB 1318 CCGTCCAGCTGAGCCCTCAGGCTTCTGCGGTGAAGAACTGCGGTTTGAGGATTTTGG 1377
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QY 1441 GAGGTGAGGCTGTGCTTATGATGAGAGAGAGTGTGAGCTGAGACTCAGAGA 1500
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DB 1438 GAGGTGAGGCTGTGCTTATGATGAGAGAGAGTGTGAGCTGAGACTCAGAGA 1497

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1561 TTGGAGCAAGCAGCGATGAGGTGTCCAGAGGATGACAAAGCATCTGAGCTTCTCAT 1620
1558 TTGGAGCAAGCAGCGATGAGGTGTCCAGAGGATGACAAAGCATCTGAGCTTCTCAT 1617
1621 GATTATCAGAGCAGAGCCCGGAAGCTCCAGAAATTTAAAGACAGAGATACAGAGCTCA 1680
1618 GATTATCAGAGCAGAGCCCGGAAGCTCCAGAAATTTAAAGACAGAGATACAGAGCTCA 1677
1681 GTGGAAGAAATGAGTTGATGATGAATCAGTTGGAAGAGATCTTGCTCAGCAAGAGA 1740
1678 GTGGAAGAAATGAGTTGATGATGAATCAGTTGGAAGAGATCTTGCTCAGCAAGAGA 1737
1741 CGGAGTGAATCTTACGAATCTGAGCTGAGAGAGTCTCGGCTTGCTGCTGAAGAAATTCAG 1800
1738 CGGAGTGAATCTTACGAATCTGAGCTGAGAGAGTCTCGGCTTGCTGCTGAAGAAATTCAG 1797
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1921 CTCGAAGAAACTGGAAGAGCTG----- 1945
1918 CTCGAAGAAACTGGAAGAGCTGTAAGAGCAGACCGAGAGCACTGAGCTGTCAG 1977
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1978 AATATCCGCGCAGGCAAGAGGAGCGAGCGAGAGGCTGGAAGTGTGAGAACCGAGAG 2037
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2218 AAACATCGGAGAGCCCAAGTCTCAGCCGAGCCTAGAGATGACCTGAAACAGAAAGAG 2277
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2353 ATTCTCAGCGAAACAGAGGCGATGATCAATGCTATGATTCCAGATCAGATCCCTGGA 2412
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2533 CTGAGACACAGGCTGGGAAGTTGAGGCCCAAGAACAGAAACTGAGAGAGCAGCTGAG 2592

2578 CTGAGACACAGGCTGGGAAGTTGAGAGGCCCAAGAACGAAACTGAGAGAGCAGCTGAG 2637
2593 AAGATCAGCCACCAAGACCAAGTGAAGAAATCGGCTGTGGAACTGAGACAAGATTTG 2652
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2773 GCCCTGAGAGCAGCTTTCGCGAGCGAAGACAGAGCTGGAAGAGACCAAGCAGAAAGT 2832
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2953 GACAAAGCTGAACTCAACAAACCAAACTTCTATCTTGTCCAAACAACTGATGAGGCTTCT 3012
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3553 TTAAGAGAGCAGATGAGACCTGCAAGAAATATCAATTTTCGCTGACCTCAAGAGACTGCA 3612
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3613 GAAAGCTTAAGTCCGAGCTGATCTTACTGAAAGACAGAAAGAAATGACTTGAAGTATCAGCTG 3672

Db 3658 GAAGCTCTAGATCGGGCTGATCTACTGAAAGACAGAAAAGATGACTTGGAGTATCAGCTG 3717
Qy 3673 GAAAAATTCAAGTTCTTATTCTCTATGTAAGAGTGAAGTGAAGGCACTATTCTCA 3732
Db 3718 GAAAAATTCAAGTGTCTATTCTCATGAAAAGTGAAGTGAAGGCACTATTCTCA 3777
Qy 3733 CAACCAAACTCATGATTTTCTGCAAGCCAAAATGGAACCACTGCTAAAAAGAAAAG 3792
Db 3778 CAACCAAACTCATGATTTTCTGCAAGCCAAAATGGAACCACTGCTAAAAAGAAAAG -- 3835
Qy 3793 GGTATTATTAGTGAAGGAAAGAGACCTGCTTTTACCAACAGGTTCTCTGCAATAC 3852
Db 3836 -----AGGTGCTCTGCAATAC 3852
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Db 4033 ATGTGCGGTCCGCAAGAGCAACAGCCCAATGAGCTGCTGTGCGCCCGCATCAGC 4092
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Qy 4633 GCA----- 4635
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OY	5743	TCGAGCCGAGCGCGCCCGGAAAGGCCCCAGCCACCGCGAAGGCCAAGCACACCCCAACGCG	5802
Db	5893	TCGAGCCGAGCGCGCCCGGAAAGGCCCCAGCCACCGCGAAGGCCAAGCACACCCCAACGCG	5952
OY	5803	TACCGCGAGGGGGCGAGCCGAGCTGGCGAGGAGCAAAAGTCTCTGTGGCCGCGCCCTGTGAACGA	5862
Db	5953	TACCGCGAGGGGGCGAGCCGAGCTGGCGAGGAGCAAAAGTCTCTGTGGCGCGCCCTGTGAACGA	6012
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Db	6013	GAGAAATCCCCCGGCGGATCTTAGCAGCGCGGAGAGACGGTCCCGCGGAGGCTGTT	6072
OY	5923	GAAACAGACAGCAGGGGGCGGCTGGCGCGGAGACCGTAGAGACCCCGCTGCCAAGTG	5982
Db	6073	GAAACAGACACAGGGGGCGGCTGGCGCGGAGACCGTAGAGACCCCGCTGCCAAGTG	6132
OY	5983	AACCAAGGAGAGGGGCGAGATGCTCTTCACATTTTCAACGGTTAAACACTGTCACT	6037
Db	6133	AACCAAGGTGGAGCAAGTCTTACATTAATCTACAGCAGAAAACCAACTCT	6187

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RESULT 12
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; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: MacDougall, John R
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; APPLICANT: Miller, Isabelle
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; APPLICANT: Lepley, Denise M
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; APPLICANT: Shinkets, Richard A
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, NUMBER OF SEQ ID NOS: 127
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO: 8
, LENGTH: 6201
, TYPE: DNA
, ORGANISM: Homo sapiens
US-09-964-956-8

Query Match          91.4%   Score 5629.8   DB 11;   Length 6201;
Best Local Similarity 95.7%   Pred. No. 0;
Matches 5929;   Conservative 0;   Mismatches 22;   Indels 246;   Gaps 4

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Qy	61	GCCAGCGCGGCGCTCCAGGCTGAATCTGTCTCCAGGGGAAACCAACCTTTATAGCTCAA	120
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Qy	121	CAGCAGATGTCCTCCTCTTTCCCGAAGAGGATATTAGATGCCCTTTGTCTCTTTGAA	180
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Qy	181	GAATGACGTACAGCTGCTCTGATGGAAGATTAAAGCACTGAGCACTTTGTCCGGAATAT	240
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Qy	241	TCCGACACCATACCTGAGTTACAGAGCTCCAGGCTTCGGCAAAAGACTTCGAGTCA	300
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Qy	361	GACATCTAGTCTATGAAAGTGAAGAAAGAAAGGCTTTATTTGGCCCGAGAGAGAGTTCA	420
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Qy	481	CAGTATGCTTTTACGACCAAAAATCACCTTTATCTGATGAGAGATATCAAGCTTGAAGG	540
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QY	961	TTTTTGAATAATTCAGATGACCCCAAGTGAAGCACTTCTTGAATCTGATTTCAAGC	1020
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QY	1141	TCCTGACGATGACACCTCCCAATTTTGATGACACAGAGAAATTCGTGGGTTTCACTCT	1200
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Db	1258	TACACAAAGGCACTGGGGAATTTCTTGATAGATCTGAGTCTGTGTGTCCGGTCTGGAATCC	1317
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Db	1378	TCCTCAGGACAAAGTGTCACAAGTGAAGCAGAGAAATGACCCGGTTACATCGAGAGCTGTCA	1437
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Db	1678	GTGGAAGAAATGAGGTTGATGATGAAATCAGTTGAAAGAGATCTTGTCTCAGCAAGAAAGA	1737
QY	1741	CGAGATGATCTTCAAGAACTTGAGCTGAGAGAGTCTCGGCTTGTCTGTAAGAAATTCAG	1800
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QY	1801	CGGAAAGGCAAGAAATGTCAGATTAACCTGTTGAAGGCTTAAGGATCAAGGAGGCTGAA	1866
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QY	1861	GTGGAGAGATATGCGAATACTGGAAGAAATCAATGCTGAGACAGACTCAAAATTCAGAG	1920
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Db	1918	CTCCAGAGAAACTGAGAGAGGCTGTAAAGCCAGCACGAGGCCACCGAGCTGCTGAC	1977
Oy	1945	-----GCAAAGAGCCGAGCCGAGAGGAGCTGAGAACTGCAGAACCGAGAG	1992
Db	1978	AATATCCGCCACGCAAGAGACCGAGCCGAGAGGGAGCTGAGAAAGCTGCAGAACCGAGAG	2037
Oy	1993	GATTCTTCTGAGGCATCAGAAAGAGCTGGTGAAGCTGAGAAACGCCCATCTTCTG	2052
Db	2038	GATTCTTCTGAGGCATCAGAAAGAGCTGGTGAAGCTGAGAAACGCCCATCTTCTG	2097
Oy	2053	GAGAAACAAGCTAAAGACATGAGACCATGAGAGGTGAGAAACAACAATGAAAGATGAC	2112
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Db	2278	CAGCACTATGAGGAAAAAGATTAAAGTGTGGAACAATCAGATTAAGAAAGACCTGGCTGAC	2337
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Oy	2353	ATTCTCAGCGAACAAGAGCGATGATCAATGCTATGGAATTCAGAGATCAGATCCCTGGAA	2412
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Oy	2413	CAGAGGATTTGGAACTGTCTGAAAGCCAAATACTTGCAGCAATATAGCAGCTTTTATAC	2472
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Db	2518	CAAGGAAACATGAAGGCGCCAAAGAGATGATTTCTGAACTCAGAGCAACAGAAATTTTAC	2577
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Oy	2593	AAGATCAGCCACCAAGACCCACAGTGAACAAGATGGCTGTGAACTGAGAGCAAGATTG	2652
Db	2638	AAGATCAGCCACCAAGACCCACAGTGAACAAGATGGCTGTGAACTGAGAGCAAGATTG	2697
Oy	2653	CGGAGAGTCAAGTCTAGAGCACAGAGACAGAAACTGAGAGCTCAAGCCCGACCTCACAGAG	2712
Db	2698	CGGAGAGTCAAGTCTAGAGCACAGAGACAGAAACTGAGAGCTCAAGCCCGACCTCACAGAG	2757
Oy	2713	CTAAGCTCTTCCCTGCAGAGCGGAGATCAACGTTGACAGCCCTGCAGAGCTGCACGGGCG	2772
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Oy	2893	CTTGATTAACAGCTGTACTGTATATACAGAGCTTGAGAGAGCAGCTTAACAGCTGACCGAG	2952
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Db 3538 CAGCAGAACTGAGAGCTGAGAGAGAGCTCAAAACAGAGGCTTGTGAAGACAGCAAA 3597
QY 3553 TTACAGACAGATGAGCTGACGAAATAATCATTTTCCGTCTGACTCAAGGACTGCA 3612
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Db 3718 GAAAACATTCAAGTTCTCTATTCTCATGAAAAGTGAATAAGAGGCACTATTCTCA 3777
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Db 3836 -----AGGTGCTCTGACGATC 3852
QY 3853 AATGAGCTGAGCTGGCCCTGAGAGAGAGAAAGCTCGCTGTGACAGACTTAAGAGAGCC 3912
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QY 3913 CTTGAGAGAGACCCGATCGAGCTCGGTCGCGCCGGAGAGAGTGGCCACCGCAAGGA 3972
Db 3913 CTTGAGAGAGACCCGATCGAGCTCGGTCGCGCCGGAGAGAGTGGCCACCGCAAGGA 3972
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QY 4033 ATCGAGCGGTGGCGAGAGACAGAGCCAGTGCATGAGAGCTGTGCCCCCGCATCCAGC 4092
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QY 4213 TGTCTGATACCGTGACCTTTGAGCGCAGGATCCAAATGTCTGAAATGTCAGGTGATG 4272
Db 4213 TGTCTGATACCGTGACCTTTGAGCGCAGGATCCAAATGTCTGAAATGTCAGGTGATG 4272
QY 4273 TGTCAACCCAGATGTCCACGCTTGCACGCACTGCGGCTTCCGCTGCTGAATATGCC 4332
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QY 4333 ACACACTTCAACGAGGCTTCTGCGGTGACAAATGAACTCCCAAGTCTCCAGACCAAG 4392
Db 4333 ACACACTTCAACGAGGCTTCTGCGGTGACAAATGAACTCCCAAGTCTCCAGACCAAG 4392
QY 4393 GAGCCAGACGAGCTTGAACCTGGAAGGTTGATGAAGTGTGCCAGATTAACAAGCA 4452
Db 4393 GAGCCAGACGAGCTTGAACCTGGAAGGTTGATGAAGTGTGCCAGATTAACAAGCA 4452
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Db 4513 GACAAATGAAGCCAGAGAGCTGGAACAGAGCCGTTGAGAAATTTAGCTGTGCTTCCC 4572
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Db 4573 GAGCGGATGTATCTATTCAATGTGCGTGTGCTTCCGAATCTGCAAAATACAGCCAA 4632
QY 4633 GCA----- 4635
Db 4633 GCAATGTCCATACATCTGAAGATGAAATCTACCCGACACCACTGCTGCGCCGGG 4692
QY 4636 ----- 4635
Db 4693 AGAACCTCTTACTTGTCTGCTCCAGCTTCCCTGACAAACAGCGCTGGTACCGCTTAA 4752
QY 4636 -----GAAAAAGCAGAGCTGATGCTTAACTG 4662
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Db 4783 TTGAAAACTCCCTTAAACCAATGTCACAGAAATTTGAGAGATCTTCCAAATTTATATATC 4992
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QY 4993 GTGAAAGAAAGTGAAGAGTCCCTGCGCCAGTCCCACTGCTGCGCCAGCCGACATCTCA 5112
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QY 5143 TTCACCAATATCTGATCCGAAAGAGATAGACCTCAGAGCCCTGACAGTATCCAC 5202
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QY 5503 GGGAGCCCTGCGGAGGCTTCTGTGACATCTCCGAGCCGCGCTACTGCGGCTGTGCANT 5562
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Db 5653 GGGAGCCCTGCGGAGGCTTCTGTGACATCTCCGAGCCGCGCTACTGCGGCTGTGCANT 5712
QY 5563 TCCTGAGAGCGATTTACTTGGGCTCTCTATACGAGATTAATTAAGGCTATTTGCTGC 5622
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QY 5623 AAGGGAACCTCTGTGAAGAGTCCGCGACTGAAACACACCGGCGGCTGTCCACTCCGC 5682
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Db 5773 AAGGGAACCTCTGTGAAGAGTCCGCGACTGAAACACACCGGCGGCTGTCCACTCCGC 5832
QY 5683 AGGAGCCCAACAGGAGGCGCCACCGACGTACACGAGACATCACCAAGCGCGTGGCC 5742
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QY 5923 GAAAGACGAGGAGGCGGCGGCTGCTGGGAGGCGGAGGCGGCGGCTGCTGCGAGGAG 5982
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QY 5983 AACCAAGGAGAGGCGCA 5999
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RESULT 13
 US-10-262-511-13
 ; Sequence 13, Application US/10262511
 ; Publication No. US20040038223A1

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; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Miller, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Paturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomti R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyanar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 13
; LENGTH: 6201
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (6198)
US-10-262-511-13

Query Match 91.4%; Score 5629.8; DB 17; Length 6201;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 5929; Conservative 0; Mismatches 22; Indels 246; Gaps 4;

QY 1 ATGTGAAGTTCAATATGAGAGCGGAGATCTTTGATGCTGTGTGTAACCCATT 60
Db 1 ATGTGAAGTTCAATATGAGAGCGGAGATCTTTGATGCTGTGTGTAACCCATT 60

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Db	61	GCCAGCCGGGCTTCAGGCTGAATCTGTCTTCCAGGGGAAACCACTTATGACTCAA	120
QY	121	CACAGATGTCTCTCTTCCCGAAGAGGATATGATGCCCTCTTGTCTCTTGAA	180
Db	121	CACAGATGTCTCTCTTCCCGAAGAGGATATGATGCCCTCTTGTCTCTTGAA	180
QY	181	GAAATGACAGCTGTCTGTATGAAGATTAGACCTGACAACTTGTCCGGAAGTAT	240
Db	181	GAATGACAGCTGTCTGTATGAAGATTAGACCTGACAACTTGTCCGGAAGTAT	240
QY	241	TCCGACACCACTACTAGTTACAGAGCTCAACCTTCGCAAAAGACTTCGAATGACA	300
Db	241	TCCGACACCACTACTAGTTACAGAGCTCAACCTTCGCAAAAGACTTCGAATGACA	300
QY	301	AGCTCTGAGGTGTGGTCACTTTCGTAAGTACAGGTGTAGAGAAAGCAACCGG	360
Db	301	AGCTCTGAGGTGTGGTCACTTTCGTAAGTACAGGTGTAGAGAAAGCAACCGG	360
QY	361	GACATCTATGCTATGAAGTGAAGAAAGGCTTTATTTGGCCAGAGCAGTTTCA	420
Db	361	GACATCTATGCTATGAAGTGAAGAAAGGCTTTATTTGGCCAGAGCAGTTTCA	420
QY	421	TTTTTGGAGAAAGGCGAACATATATCTCCAGACAAAGCCCTGTGATCCCCCAATTA	480
Db	421	TTTTTGGAGAAAGGCGAACATATATCTCCAGACAAAGCCCTGTGATCCCCCAATTA	480
QY	481	CAGTATGCTTTTCAGGACAAAATCACTTTATCTGATGAGGAATATCAGCTTGAAGG	540
Db	481	CAGTATGCTTTTCAGGACAAAATCACTTTATCTGATGAGGAATATCAGCTTGAAGG	540
QY	541	GACTGTCTCTCACTTTTGAATAGATATGAGACCACTTATGATGAACCTGATACAGTT	600
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Db	601	TACTAGTCACTGATTTTGGCTGTTCACAGGTTCACTGATGGGATACGTGACTGCA	660
QY	661	GACATCAAGCTTGAGAACATCTCTGTTGACCGCAACGACATCAAGCTGTGTGATTT	720
Db	661	GACATCAAGCTTGAGAACATCTCTGTTGACCGCAACGACATCAAGCTGTGTGATTT	720
QY	721	GGATCTGCGGGAATGAATTCAAACAGAGGTGAAGCCAACTCCCATTTGGGACC	780
Db	721	GGATCTGCGGGAATGAATTCAAACAGAGGTGAAGCCAACTCCCATTTGGGACC	777
QY	781	CCAGATTACATGAGCTCTGAAAGTGTGACTGTGATGAACGCGGATGAAAAAGCACTAC	840
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QY	841	GCCCTGGAAGTGTGACTGTGTGACTGTGGGCTGATTCCTATGAGATGATTTATGGAGA	900
Db	838	GCCCTGGAAGTGTGACTGTGTGACTGTGGGCTGATTCCTATGAGATGATTTATGGAGA	897
QY	901	TCCCCCTTCGACAGAGGAACCTCTGCGCAAGCTTCAATTAATATGAATTTCCAGCG	960
Db	898	TCCCCCTTCGACAGAGGAACCTCTGCGCAAGCTTCAATTAATATGAATTTCCAGCG	957
QY	961	TTTTTGAATTTCCAGATGACCCCAAGGTGACAGTGACTTCTTGATCTGATTCAAAGC	1020
Db	958	TTTTTGAATTTCCAGATGACCCCAAGGTGACAGTGACTTCTTGATCTGATTCAAAGC	1017
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Qy	1201	CCGTGCAAGCTGAGCCCTCTCAGGCTTCTCGGATGAAGAACTGCGGTTGTGGGGTTTTCG	1260
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Qy	1261	TACAGAAAGGCACTGGGGATTTTGTGTGATCTTGAGCTTGTTTGTGTGGGTTCTGACTCC	1320
Db	1258	TACAGAAAGGCACTGGGGATTTTGTGTGATCTTGAGCTTGTTTGTGTGGGTTCTGACTCC	1317
Qy	1321	CCTGCCAAAGCTAGGCTCCATGGAAAAAGAACTTTCATCAAAAGCAAGAGCTCAAGAC	1380
Db	1318	CCTGCCAAAGCTAGGCTCCATGGAAAAAGAACTTTCATCAAAAGCAAGAGCTCAAGAC	1377
Qy	1381	TCTCAGAGCAAGTGTCAACAGATGAGCAGGAAATGACCCGGTTACATCGAGAGTGTCA	1440
Db	1378	TCTCAGAGCAAGTGTCAACAGATGAGCAGGAAATGACCCGGTTACATCGAGAGTGTCA	1437
Qy	1441	GAGGTGAGGCGTGTGCTTAATCAGAAAGGATGGAGCTGAAGGCTCTGAGCTCAGAGA	1500
Db	1438	GAGGTGAGGCGTGTGCTTAATCAGAAAGGATGGAGCTGAAGGCTCTGAGCTCAGAGA	1497
Qy	1501	TCCCTCTGAGCAGAGCCCTTGCTACCTACATCAACAGATGCAAGTACTTAAAGCGAAGT	1560
Db	1498	TCCCTCTGAGCAGAGCCCTTGCTACCTACATCAACAGATGCAAGTACTTAAAGCGAAGT	1557
Qy	1561	TTGGAGCAAGGCAACGGATGAGAGGTGTCCAGAGAGATGACAAAGCATGCGACTTCTCAT	1620
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Qy	1621	GATATCAGAGAGCAGAGCCGGAACCTCCAGAAATCAAAGAGCAGAGTACCAAGGCTCAA	1680
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Qy	1681	GTGGAAGAAATGAGGTTGATGATGAATCAAGTTGGAAAGGATCTTGTCTCAGCAAGAGAG	1740
Db	1678	GTGGAAGAAATGAGGTTGATGATGAATCAAGTTGGAAAGGATCTTGTCTCAGCAAGAGAG	1737
Qy	1741	CGAGTGAATCTCTACGAACTCGAAGCTGAGAGGCTCGGCTTGCTGTAAGAAATTCAG	1800
Db	1738	CGAGTGAATCTCTACGAACTCGAAGCTGAGAGGCTCGGCTTGCTGTAAGAAATTCAG	1797
Qy	1801	CGGAAAGCGACAGATGTCAAGATPAACTGTGGAAGGCTAAGGATCAAGGAGCCTGGA	1860
Db	1798	CGGAAAGCGACAGATGTCAAGATPAACTGTGGAAGGCTAAGGATCAAGGAGCCTGGA	1857
Qy	1861	GTGGGAGAAATGTGGGAACTGAGAGAAATCAATGATCTGAGCAGAGCTCAAAATTCAGAG	1920
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Qy	1921	CTCCAAAGAAACTGAGAAAGGCT-----	1944
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Qy	1945	-----GCAAGGAGCCGAGCCGAGAGGAGCTGAGAGAGCTGACAGACCTGAGAG	1992
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Qy	1993	GATTCTTCTGAGGCACTCAAGAAAGAGCTGTGTGGAAGCTGAGGAAAGCCGCCATTCTCG	2052
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Qy	2053	GAGAACAGGTTAAAGACTTAGAGCACTGAGCCTTAGAGAAACAGACTGAGAGATGAC	2112
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2758 CTACAGCTCTCCCTGACAGAGCGAGTCA CAGTTGACAGCCCTGAGGCTGACAGGAG 2817
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3058 GGGGCCAAGAGAGATTGTATCAACTGCGAAGTGAAGTGAACATCTCCGCGGAGATC 3117
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3178 TGACCATGCTGAGAGAAAGGT CATGATTTGAGAGCCCTTAAACATGAGCTGTAGAA 3237
3193 AAAAGACGAGAGTGGAGGCTTGGAGAGAGTCTTGGGTGATGAGAAATCCAGTTTGG 3252
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3778 CAAACCAATCAATTGATTTTCTGCAAGCCAAATGAGCAACTGCTTAAAGAAAAAG 3835
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3836 -----AGGTGCTCTGACAGTAC 3852
3853 AATGAGCTGAAGCTGGCCCTGAGAAAGAGAAAGCTCGCTGTCAGAGCTTAAGAGAGCC 3912
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3913 CTTCGAAGACCCGATGAGGCTCCGGTCCGCGCGGAGAGAGCTGCCACCGCAAGGA 3972
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4093 CGCAGAAAGAGTCTTCACTCAGAGAAATTTAGTCCGCTCTTAAGAAAGCATGAC 4152
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QY	4393	GAGCCACGACGACGCTTGGACCTGGAGGGGTGGATGAAAGTGTCCACGAAATPACAAACGA	4452
Db	4393	GAGCCACGACGACGCTTGGACCTGGAGGGGTGGAGAAAGTGTCCACGAAATPACAAACGA	4452
QY	4453	GGAACGACAAGGCTGGGACAGAAAGTACATTTGTCTGTGGAGGGATCAAAAGTCTCTCATTTAT	4512
Db	4453	GGAACGACAAGGCTGGGACAGAAAGTACATTTGTCTGTGGAGGGATCAAAAGTCTCTCATTTAT	4512
QY	4513	GAACAATGAAAGCCAGAGAAAGCTGGACAGAGAGCCGTGGAAAGAAATTTGAAGCTGTGCTTCC	4572
Db	4513	GAACAATGAAAGCCAGAGAAAGCTGGACAGAGAGCCGTGGAAAGAAATTTGAAGCTGTGCTTCC	4572
QY	4573	GACGGGGAATGTATCTATTTCAATTCATGATGATGCTTGGTGTCTTCGAACTGTGCAAAATPACGCAAA	4632
Db	4573	GACGGGGAATGTATCTATTTCAATTTCAATTTGATGCTTGGTGTCTTCGAACTGTGCAAAATPACGCAAA	4632
QY	4633	GCA-----	4635
Db	4633	GCAAGATGTCATATACATACATACTGAAGATGAAATCTCACCCGACACCACTGTGTGCGCGG	4692
QY	4636	-----	4635
Db	4693	AGAACCTCTACTTGTCTAGCTTCCAGCTTCCCTGCAAAACAGCGTGGGTACCGCCTTA	4752
QY	4636	-----GAAAAAGCAGAAAGCTGATGCTAAACTG	4662
Db	4753	GAATCAGTTGTTCGAGGGTGGAGAGATTTCTAGGGAAAAAGCAGAAAGCTGATGCTAAACTG	4812
QY	4663	CTTGGAAACTCCCTCTCTGAAACTGGAAAGTATGAACGCTCTAGACATGAACTGCAACGCTG	4722
Db	4813	CTTGGAAACTCCCTCTCTGAAACTGGAAAGTATGAACGCTCTAGACATGAACTGCAACGCTG	4872
QY	4723	CCCTTCAGTGAACGAGTGTGTGTGGTGGGACCCAGAGAAAGGGCTCTAGCGCCCTGAATGTC	4782
Db	4873	CCCTTCAGTGAACGAGTGTGTGTGGTGGGACCCAGAGAAAGGGCTCTAGCGCCCTGAATGTC	4932
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Db	4933	TTGAAAACTCCCTTAAACCATGTCCAGAAATTTGAGACGTCCTTCAAAATTTATATATTC	4992
QY	4843	AAAGACCTGGAGAAAGCTACTCATATATACAGAGAAAGACGGGACCTGTGTCTTGTGGAC	4902
Db	4993	AAAGACCTGGAGAAAGCTACTCATATATACAGAGAAAGACGGGACCTGTGTCTTGTGGAC	5052
QY	4903	GTGAAGAAAGTGAACAGTCCCTGGCCACAGTCCACCTGACCTGACCCGACCATCTCA	4962
Db	5053	GTGAAGAAAGTGAACAGTCCCTGGCCACAGTCCACCTGACCTGACCCGACCATCTCA	5112
QY	4963	CCCAACATTTTGAAGCTGTCAAGGGCTGCCACTTTGTTGGGGCAGGCAAGATTGAGAAC	5022
Db	5113	CCCAACATTTTGAAGCTGTCAAGGGCTGCCACTTTGTTGGGGCAGGCAAGATTGAGAAC	5172
QY	5023	GAGGCTGTGCATCTGTGACGACCATGCCCCAGCAAAATCTGCAATTCCTCCGCTTCAACGAAAC	5082
Db	5173	GAGGCTGTGCATCTGTGACGACCATGCCCCAGCAAAATCTGCAATTCCTCCGCTTCAACGAAAC	5232
QY	5083	CTCAGCAAAATCTGTGATCCGAAAAAGATAGAGACCTCAGAGCCCTTGACCTGTATTCAC	5142
Db	5233	CTCAGCAAAATCTGTGATCCGAAAAAGATAGAGACCTCAGAGCCCTTGACCTGTATTCAC	5292
QY	5143	TTTCAACCAATTAACGATATCTCATTTGGAAACCAATTAATTTCTACGAAATTCGACATGAGACAG	5202
Db	5293	TTTCAACCAATTAACGATATCTCATTTGGAAACCAATTAATTTCTACGAAATTCGACATGAGACAG	5352
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Db	5353	TACACGCTCGAGGAATCTGTGATTAAGATGACCAATTCCTTGGACCTGTGCTGTGTTGAC	5412
QY	5263	GCCCTTTTCCAAACAGCTTCCCTGTCTCAATGTGTGACGTTAAACAGCGGACGACGAG	5322
Db	5413	GCCCTTTTCCAAACAGCTTCCCTGTCTCAATGTGTGACGTTAAACAGCGGACGACGAG	5472

QY	5323	GAGCTATTGCTGTTGTTTCCACGAATTTGGAGTCTTGATGATCTTAAACGAACGTAAC	5382
Db	5473	GAGTACTTCTGTTGTTCCACGAATTTGAGTGTGTGATATTTAAACGAACGTAAC	5532
QY	5383	CGCACAGACGATCTCAAGTGAAGTGGCTTACCTTTGGCTTTGCTTACAGAGAACCTTAT	5442
Db	5533	CCACAGACGATCTCAAGTGAAGTGGCTTAACTTTGGCTTTGCTTACAGAGAACCTTAT	5592
QY	5443	CTGTTTGTGACCCACTTCAACTCACTGAAAGTAATTGAATTCAGGCAAGCTCTTACGCA	5502
Db	5593	CTGTTTGTGACCCACTTCAACTCACTGAAAGTAATTGAATTCAGGCAAGCTCTTACGCA	5652
QY	5503	GGGACCCCTGACCCGAGCGTACCTGGACATCCCGAAACCCGCGTACCTGGAGCCCTGACAT	5562
Db	5653	GGGACCCCTGACCCGAGCGTACCTGGACATCCCGAAACCCGCGTACCTGGAGCCCTGACAT	5712
QY	5563	TCCTCAGAGACGATTTTACTTGGCGTCTCATACAGAGATPAATTAAAGGTCATTTGCTGC	5622
Db	5713	TCCTCAGAGACGATTTTACTTGGCGTCTCATACAGAGATPAATTAAAGGTCATTTGCTGC	5772
QY	5623	AAGGGAACCTGTGTGAAGGAGTCCGGCACTGAACCAACCGGGGCGCGTCCACTCCCGC	5682
Db	5773	AAGGGAACCTGTGTGAAGGAGTCCGGCACTGAACCAACCGGGGCGCGTCCACTCCCGC	5832
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Db	5833	AGCAGCCCCCAACAGCGAGGCCAACCCAGTACAAACGAGCAATCAACCAAGCGCGTGGCC	5892
QY	5743	TCCACCCCGAGCGCCCGGCAAGGCCCGCAAGCCACCCGCGAGACCCAGCAACCCCAACCGC	5802
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QY	5803	TACCGCGAGGGCGGACCGAGCTGCGCAGGGACAAGTCTCTGCGCGCCCCCTGAGAGCA	5862
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QY	5863	GAGAAGTCCCCCGGCGCGGATGTCTACGACCGCGGAAGAGCGGTCCCCCGGAGAGCTGTTT	5922
Db	6013	GAGAAGTCCCCCGGCGCGGATGTCTACGACCGCGGAAGAGCGGTCCCCCGGAGAGCTGTTT	6072
QY	5923	GAAAGCACAGCAGAGGGGCGCGGCTGCTGCGGGAGCGAGAGACCCCGCTGAACCAAGTTG	5982
Db	6073	GAAAGCACAGCAGAGGGGCGCGGCTGCTGCGGGAGCGAGAGACCCCGCTGAACCAAGTTG	6132
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Db	6133	AACAAAGTGAAGGCA 6149	

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RESULT 14
US-10-028-946-3
; Sequence 3, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-3

Query Match      87.0%; Score 5358; DB 13; Length 5877;
Best Local Similarity 95.8%; Pred. No. 0;

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Matches 5634; Conservative 0; Mismatches 5; Indels 243; Gaps 3;

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DB 1 AGTTGAAGTTAAATATGAGCGGGAAATCCTTGGATGCTGAGTCCATC 60
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DB 61 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCACTTTATGACTCA 120
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DB 121 CAGCAGATGTCCTCTCTTCCGAGAGGAGATTAAGATGCCCTTTGTTCTTTGAA 180
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 QY 4513 GACAAATGAAGCCAGAGAAAGTGTGACAGAGGCGGTGGAAGAAATTTGAGCTGTGCTTCC 4572
 Db 4516 GACAAATGAAGCCAGAGAAAGTGTGACAGAGGCGGTGGAAGAAATTTGAGCTGTGCTTCC 4575
 QY 4573 GACGGGGATGTATCTATTGCTGAGTGGCGTTGATGCTTCCGAATCTCGCAATACAGCCAA 4632
 Db 4576 GACGGGGATGTATCTATTGCTGAGTGGCGTTGATGCTTCCGAATCTCGCAATACAGCCAA 4635
 QY 4633 GCA----- 4635
 Db 4636 GGAATGTCCCATACATTAAGATGAATCTCACCCGACACACTGTGCGCCGG 4695
 QY 4636 ----- 4635
 Db 4696 AGAACCTCTACTTGTAGTCTCCAGCTTCCCTGACAAACAGCGTGGGTCAACCGCTTA 4755
 QY 4636 ----- 4662
 Db 4756 GAATCATGTTGTCCAGAGTGGAGAGTTTCTAGGAGAAAGACAGAACTGATGCTTAACCTG 4815
 QY 4663 CTTGAAATCTCCCTGCTGAAATCTGAAGGTATGACCTGTACATGAACTGACGCTG 4722
 Db 4816 CTTGAAATCTCCCTGCTGAAATCTGAAGGTATGACCTGTACATGAACTGACGCTG 4875
 QY 4723 CCCTTCACTGACAGAGTGTGTGTGGGACCTGAGAGAGGGCTTACCGCTGAAATGTC 4782
 Db 4876 CCCTTCACTGACAGAGTGTGTGTGGGACCTGAGAGAGGGCTTACCGCTGAAATGTC 4935
 QY 4783 TTGAAATCTCCCTAATCCATGTCAGAGAAATGAGAGTCTTCCAAATTAATATATTC 4842
 Db 4936 TTGAAATCTCCCTAATCCATGTCAGAGAAATGAGAGTCTTCCAAATTAATATATTC 4995
 QY 4843 AAGSACCTGAGAGAGTACTCATATGATAGCAGAGAGAGGAGCACTGTGTCTTGTGAC 4902
 Db 4996 AAGSACCTGAGAGAGTACTCATATGATAGCAGAGAGAGGAGCACTGTGTCTTGTGAC 5055
 QY 4903 GTGAGAAAGTGAACAGTCTCCTGAGTCCAGTCCACCTGCTTGCAGCCGACATCTCA 4962
 Db 5056 GTGAGAAAGTGAACAGTCTCCTGAGTCCAGTCCACCTGCTTGCAGCCGACATCTCA 5115
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 QY 5143 TTCACCAATTAATCTGATCTCGGAAAGATAGAGACTCAGAGCCTGACGCTGTATCCAC 5202
 Db 5296 TTCACCAATTAATCTGATCTCGGAAAGATAGAGACTCAGAGCCTGACGCTGTATCCAC 5355
 QY 5203 TACACGCTGAGAGAAATTCCTGATTAAGAAATGACCATTCCTTGGACCTGCTGTGTC 5262
 Db 5356 TACACGCTGAGAGAAATTCCTGATTAAGAAATGACCATTCCTTGGACCTGCTGTGTC 5415

QY 5263 GCCTCTTCCAGAGCTTCCCTGTCTCAATGCTGACAGTGAACAGGCGAGGGAGAGAG 5322
 Db 5416 GCCTCTTCCAGAGCTTCCCTGTCTCAATGCTGACAGTGAACAGGCGAGGGAGAGAG 5475
 QY 5323 GAGTACTTGTGTGTTTCCAGCAATTTGAGTGTGTGTGATTTCTTACCGAAGAGTAC 5382
 Db 5476 GAGTACTTGTGTGTTTCCAGCAATTTGAGTGTGTGTGATTTCTTACCGAAGAGTAC 5535
 QY 5383 GCGACAGAGATCTCAAGTGAAGTGTGCTTACCTTTGGCTTTGCTTACAGAGACCTAT 5442
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 Db 5596 CTTGTTGACCCCACTTGAACCTCACTCGAAGTAATGAGATTCAGAGACGCTTCAGCA 5655
 QY 5503 GGGACCCCTGCGCGAGCTGACATCCGAAACCGGCTTACCTGGGCGCTGCAAT 5562
 Db 5656 GGGACCCCTGCGCGAGCTGACATCCGAAACCGGCTTACCTGGGCGCTGCAAT 5715
 QY 5563 TCCTCAGAGCGATTTACTTGGCGTCTCATACAGATTAATTAAGGCTCATTTGCTGC 5622
 Db 5716 TCCTCAGAGCGATTTACTTGGCGTCTCATACAGATTAATTAAGGCTCATTTGCTGC 5775
 QY 5623 AAGGAAACCTGTGAAGAGTCCGCACTGAACACACCGGGGCGCTTCCACCTCCGC 5682
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 QY 5683 AG 5684
 Db 5836 AG 5837

RESULT 15
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 ; Publication No. US20040209297A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, Xuanchuan
 ; APPLICANT: Miranda, Maricar
 ; APPLICANT: Fridge, Carl Johan
 ; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0289-USA
 ; CURRENT APPLICATION NUMBER: US/10/791,666
 ; PRIOR FILING DATE: 2004-03-02
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: US 60/258,335
 ; PRIOR FILING DATE: 2000-12-27
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5877
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-791-666-3

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 QY 121 CAGCAGATGTCTCTCTTCCGAGAGAGGATATAGATGCGCTTGTGCTTTGAA 180
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QY	241	TCCGACACATTAAGCTGATTAACAGAGCTCCAGCCTTGGCAAAAGCACTTGAAGTCAGA	300
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QY	301	AGCTTTGAGGTTTGTCATCTTGTCTGAAGTCAGGTGGTAAAGAGAAAGCAACGGG	360
Db	301	AGCTTTGAGGTTTGTCATCTTGTCTGAAGTCAGGTGGTAAAGAGAAAGCAACGGG	360
QY	361	GACATCTATGCTATGAAGAAGTATGAAGAAGAGGCTTTATTTGGCCAGAGACAGTTTCA	420
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QY	421	TTTTTTGAGGAAGACGGGAACATATTATCTGAAGCAAGACCCGTGGATCCCCCAATT	480
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QY	481	CAGTATGCCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCTGGAGGG	540
Db	481	CAGTATGCCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCTGGAGGG	540
QY	541	GACTTGTGTCACTTTGAATATGATATGAGAGCACATGTAATGAAAACCTGATATCAGTTT	600
Db	541	GACTTGTGTCACTTTGAATATGATATGAGAGCACATGTAATGAAAACCTGATATCAGTTT	600
QY	601	TACCTAGCTAGCTGATTTTGGCTGTTTCACAGCGTTCATCTGAATGGGATACGGTCAATGA	660
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Db	661	GACATCAAGCTGAGAACATTTCTCTGTGACCGCACAGACACATCAAGCTGGTGAATTTT	720
QY	721	GGATCTGCCGCAAAATGAAATTAACAAGATGTGAATGCCAACTCCCGAATGGGAGAC	780
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QY	781	CCAGATTAAATGGCTCTCTGAAGTCTGACTGTGATGAACGGGAGATGAAAAGCACTTAC	840
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QY	901	TCCCCCTTGGCAGAGGGAACCTCTGCAGAACCTTCAATTAATTTATGAAATTTCCAGCG	960
Db	901	TCCCCCTTGGCAGAGGGAACCTCTGCAGAACCTTCAATTAATTTATGAAATTTCCAGCG	960
QY	961	TTTTTGAATTTCCAGATGACCCCAAGGAGACATGACTTCTTGATCTGATCTGAANGC	1020
Db	961	TTTTTGAATTTCCAGATGACCCCAAGGAGACATGACTTCTTGATCTGATCTGAANGC	1020
QY	1021	TTGTTGTGGGCGCAGAAAAGAGACTGAAGTTTGAAGTCTTGTGTCATCTCTTCTC	1080
Db	1021	TTGTTGTGGGCGCAGAAAAGAGACTGAAGTTTGAAGTCTTGTGTCATCTCTTCTC	1080
QY	1081	TCTAAATTTGACTGGAACAACTTGTAACTCTCTCCCCCTTGCTGCCACCTCAAG	1140
Db	1081	TCTAAATTTGACTGGAACAACTTGTAACTCTCTCCCCCTTGCTGCCACCTCAAG	1140
QY	1141	TCTGACATGACACCTCCAAATTTTATGAACACAGAGAAATTTGGGGTTTCACTCCT	1200
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QY	1201	CCGTGCCAGCTGAGGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTTCG	1260
Db	1201	CCGTGCCAGCTGAGGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTTCG	1260

QY	1261	TACAGCAAGGCACTGGGAGATTCTTGGTAGTCTGAATCTGTTGTGTGGGTCTGGACTTC	1320
Db	1261	TACAGCAAGGCACTGGGAGATTCTTGGTAGCTGAATCTGTTGTGTGGGTCTGGACTTC	1320
QY	1321	CTGCGCAAGACTAGCTCATGTAGAAAAGAACTTCTCATGAAAAGCAAGAGCTCAAGAC	1380
Db	1321	CTGCGCAAGACTAGCTCATGTAGAAAAGAACTTCTCATGAAAAGCAAGAGCTCAAGAC	1380
QY	1381	TTCTCAGGACAAAGTGTCACAAATGAGCAGAGAAATGACCCGGTTAATTCGAGAGTGTCA	1440
Db	1381	TTCTCAGGACAAAGTGTCACAAATGAGCAGAGAAATGACCCGGTTAATTCGAGAGTGTCA	1440
QY	1441	GAGGTGAGGCTGTGCTTAGTCAGAGAGGAGGTGAGCTGAAGGCTTGAGACTGAGAGA	1500
Db	1441	GAGGTGAGGCTGTGCTTAGTCAGAGAGGAGGTGAGCTGAAGGCTTGAGACTGAGAGA	1500
QY	1501	TCCCTCTCTGAGCAGGACCTTGTCTACATCAAGAATGCAATGCTTAAGCGAAGT	1560
Db	1501	TCCCTCTCTGAGCAGGACCTTGTCTACATCAAGAATGCAATGCTTAAGCGAAGT	1560
QY	1561	TTGGAGCAAGCAACGATGAGGTGTCCAGAGAGATGACAAAGCACTGCAGCTTCTCAT	1620
Db	1561	TTGGAGCAAGCAACGATGAGGTGTCCAGAGAGATGACAAAGCACTGCAGCTTCTCAT	1620
QY	1621	GATATCAGAGACAGACGCCGAGGCTCCAGAAATCAAAAGCAGAGATCACAGCTTCAA	1680
Db	1621	GATATCAGAGACAGAGCCGAGGCTCCAGAAATCAAAAGCAGAGATCACAGCTTCAA	1680
QY	1681	GTGGAAAGAAATGAGGTGATGATGATCAATTGAGAGAGATCTGTCTCAGCAAGAGA	1740
Db	1681	GTGGAAAGAAATGAGGTGATGATGATCAATTGAGAGAGATCTGTCTCAGCAAGAGA	1740
QY	1741	CGAGTGAATCTTAGAAATCTGAGCTGAGAGAGTCTGGGCTTGTGCTGAAGAAATTCAG	1800
Db	1741	CGAGTGAATCTTAGAAATCTGAGCTGAGAGAGTCTGGGCTTGTGCTGAAGAAATTCAG	1800
QY	1801	CGGAAAGCGACAGAAATGTACATTAACCTGTTGAAGCTTAAGATCAAGGAGAGCTGAA	1860
Db	1801	CGGAAAGCGACAGAAATGTACATTAACCTGTTGAAGCTTAAGATCAAGGAGAGCTGAA	1860
QY	1861	GTGGAGAAATATGCGAAACTGAGAGAGTCAATCTGAGCAGCAGCTCAAAATTCAGAG	1920
Db	1861	GTGGAGAAATATGCGAAACTGAGAGAGTCAATCTGAGCAGCAGCTCAAAATTCAGAG	1920
QY	1921	CTTCAAGAGAACTGAGAGAGCT-----	1944
Db	1921	CTTCAAGAGAACTGAGAGAGAGCTGTAAAGCAGACGAGGCGACCGAGCTGTGACG	1980
QY	1945	-----GCAAGAGAGCGAGCCGAGAGGAGCTGAGAGAGCTGAGAGAGCTGCAAGCCGAGG	1992
Db	1981	AATATCCGCCAGCGAAAGAGCCGAGAGGAGCTGAGAGAGCTGCAAGCCGAGG	2040
QY	1993	GATTTCTTCTGAGGCATCAGAAAGAACTGCTGTGAGAGCTGAGGAAAGCGGCGCAATTCG	2052
Db	2041	GATTTCTTCTGAGGCATCAGAAAGAACTGCTGTGAGAGCTGAGGAAAGCGGCGCAATTCG	2100
QY	2053	GAGAAACAAGTTAAAGAGACTGAGACCAATGAGCGTTGAGAGAAACAGACTGAGAGATGAC	2112
Db	2101	GAGAAACAAGTTAAAGAGACTGAGACCAATGAGCGTTGAGAGAAACAGACTGAGAGATGAC	2160
QY	2113	ATCCAGACAAAAATCCCAACAGATCCACAGACATGAGCTGTATTAATTCGTGAGCTCGAAGG	2172
Db	2161	ATCCAGACAAAAATCCCAACAGATCCACAGACATGAGCTGTATTAATTCGTGAGCTCGAAGG	2220
QY	2173	AAACATGGGAGGCCCAAGTCTCAGCCACAGCACTTAAGATGCACTTGAAACAGAAAGG	2232
Db	2221	AAACATGGGAGGCCCAAGTCTCAGCCACAGCACTTAAGATGCACTTGAAACAGAAAGG	2280
QY	2233	CAGACATATGAGGAAAAGTTAAAGTGTGAGCAATCAATTAAGAAAGAACTGTGCTGAC	2292
Db	2281	CAGACATATGAGGAAAAGTTAAAGTGTGAGCAATCAATTAAGAAAGAACTGTGCTGAC	2340
QY	2293	AAGGAGCACTGAGAAACATGATGACAGACACAGAGAGAGGCGCATGAGAAAGGCAAA	2352

Dp	2341		AAGGAGACATCGAGAMCATGATGAGAGACAGAGGGAGGCCCATGAAAGGGCAAA	2400
Qy	2353		ATTCTCAGCGAAACAGAAAGGCGATGATCAATCTATGATATTCAGAGTTCAGATCCCTGGAA	2412
Dp	2401		ATTCTCAGCGAAACAGAAAGGCGATGATCAATCTATGATATTCAGAGTTCAGATCCCTGGAA	2460
Qy	2413		CAGAGGATTTGTGAACTGTCTTGAAAGCCAAATACTTGACGCAAAATAGCAGTCTTTTAAAC	2472
Dp	2461		CAGAGGATTTGTGAACTGTCTTGAAAGCCAAATACTTGACGCAAAATAGCAGTCTTTTAAAC	2520
Qy	2473		CAAGGAAATGAAAGGCCCAAGAAAGATGATTTTCTGAACTCAGCGCAACAAAAATTTTAC	2532
Dp	2521		CAAGGAAATGAAAGGCCCAAGAAAGATGATTTTCTGAACTCAGCGCAACAAAAATTTTAC	2580
Qy	2533		CTGAGACACACAGGCTGGAGATTGGAGGCCACAGAAACCAAAACTGAGAGACAGCTGGAG	2592
Dp	2581		CTGAGACACACAGGCTGGAGATTGGAGGCCACAGAAACCAAAACTGAGAGACAGCTGGAG	2640
Qy	2593		AAGATCAGCCACCAAGACACAGTGTACAAGAAATCGGCTTGAGAACTTGAGAACAAATTG	2652
Dp	2641		AAGATCAGCCACCAAGACACAGTGTACAAGAAATCGGCTTGAGAACTTGAGAACAAATTG	2700
Qy	2653		CGGAGGCTCACTCTTAGAGACAGAGGAGCAAGAACTGAGGCTCAAGCCGACACTCAAGAG	2712
Dp	2701		CGGAGGCTCACTCTTAGAGACAGAGGAGCAAGAACTGAGGCTCAAGCCGACACTCAAGAG	2760
Qy	2713		CTACAGCTCTCCCTGACAGAGCGGAGTCAAGTTGACAGGCCCTGACAGGCTGCACGGGCG	2772
Dp	2761		CTACAGCTCTCCCTGACAGAGCGGAGTCAAGTTGACAGGCCCTGACAGGCTGCACGGGCG	2820
Qy	2773		GCCCTGAGAGCCAGCTTCGCGAGGCGAGACAGAGCTTGAGAAAGAACCCACAGCAAGACT	2832
Dp	2821		GCCCTGAGAGCCAGCTTCGCGAGGCGAGACAGAGCTTGAGAAAGAACCCACAGCAAGACT	2880
Qy	2833		GAAAGAGGATTCAGGCACTCAAGGCACTTAGAGTGAATTCAGCGCAAAATTTGATGCT	2892
Dp	2881		GAAAGAGGATTCAGGCACTCAAGGCACTTAGAGTGAATTCAGCGCAAAATTTGATGCT	2940
Qy	2893		CTTGTTAACACTGTGACTGTATATCAACAACCTGAGAGGAGGACTTAAACACTGACCGAG	2952
Dp	2941		CTTGTTAACACTGTGACTGTATATCAACAACCTGAGAGGAGGACTTAAACACTGACCGAG	3000
Qy	2953		GACAAACGCTGAATCTCAACAAACAAACCTTCTACTGTTCTCAACAAACTCGATGAGGCTTCT	3012
Dp	3001		GACAAACGCTGAATCTCAACAAACAAACCTTCTACTGTTCTCAACAAACTCGATGAGGCTTCT	3060
Qy	3013		GGCGCGAACGACGAGATTGTACAACTGCGAAGTGAAGTGAACCATCTCCGCGGAGATC	3072
Dp	3061		GGCGCGAACGACGAGATTGTACAACTGCGAAGTGAAGTGAACCATCTCCGCGGAGATC	3120
Qy	3073		ACGGAACGAGAGATGACAGCTTACCAAGCCAGAAAGCAAAAGATGAGGCTCTGAAGACAG	3132
Dp	3121		ACGGAACGAGAGATGACAGCTTACCAAGCCAGAAAGCAAAAGATGAGGCTCTGAAGACAG	3180
Qy	3133		TGCAACCATGCTGAGAGGAAACAGGTCAATGATTTTGAGAGGCCCTTAAACGATGACTGTAA	3192
Dp	3181		TGCAACCATGCTGAGAGGAAACAGGTCAATGATTTTGAGAGGCCCTTAAACGATGACTGTAA	3240
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Qy	3253		TGTGGGTTTCAGAGACTGCAAGAAATGCTTGAAACCCAGAAACAGAGAGGCGAGAGCC	3312
Dp	3301		TGTGGGTTTCAGAGACTGCAAGAAATGCTTGAAACCCAGAAACAGAGAGGCGAGAGCC	3360
Qy	3313		GATCAGCGGATCAACGAGTCTCGCAGAGTGTGAGCTGCGACAGTGAAGAGACACAAAGCT	3372
Dp	3361		GATCAGCGGATCAACGAGTCTCGCAGAGTGTGAGCTGCGACAGTGAAGAGACACAAAGCT	3420
Qy	3373		GAGATTCCTGCTTCGACAGGCTTCAAGAGCAAGAGCTGAAGGCCGAGAGCCTCTCT	3432

Db	3421	GAGATTCTCGCTCGCAGCAGCGCTCTCAAGAGCAGAAAGCTGAAGGCCGAGAGGCTCTCT	3480
Oy	3433	GACNAGCTCAATGACCTTGAGAGAGAGACATGCTATGCTTGAAATGAAATGCCCGAAGCTTA	3492
Db	3481	GACAAGCTCAATGACCTTGAGAGAGAAACATGCTATGCTTGAAATGAAATGCCCGAAGCTTA	3540
Oy	3493	CAGCAGAAAGCTGAGACTGAAACGAGACTCAACAGAGGCTTCTGGAAGAGCAAGCCAA	3552
Db	3541	CAGCAGAAAGCTGAGACTGAAACGAGACTCAACAGAGGCTTCTGGAAGAGCAAGCCAA	3600
Oy	3553	TTACAGCAGCAGATGAGACTGCAAGAAATCACTTTTCCGTCTGACTCAAGAGCTCAA	3612
Db	3601	TTACAGCAGCAGATGAGACTGCAAGAAATCACTTTTCCGTCTGACTCAAGAGCTCAA	3660
Oy	3661	GAACTCTAGATCGGGCTGATCTACTGAAAGCAGAAAGAAAGTACTTGAGATACACTG	3720
Db	3673	GAAAAATTCAGGTTCTCTATTTCTCATGAAAAAGGTGAAAAATGAAAGGCATATTTCTCA	3732
Oy	3721	GAAAAATTCAGGTTCTCTATTTCTCATGAAAAAGGTGAAAAATGAAAGGCATATTTCTCA	3780
Oy	3733	CAAAACCAAACTCATTTGATTTTCTGCAAGCCAAAATGAGACCAACTGCTAAAAAGAAAAG	3792
Db	3781	CAAAACCAAACTCATTTGATTTTCTGCAAGCCAAAATGAGACCAACTGCTAAAAAGAAA--	3838
Oy	3793	GGTTTATTTAGTCGACGGAAGAGAGACCTTGCTTTACCAACAGTTTCTCTGACATAC	3852
Db	3839	-----AGTTTCTCTGACATAC	3855
Oy	3853	AATAGACTGAAGCTTGCCCTTGAGAGAGAGAAAGCTGCTGTGACAGCTATAGAGAAAGCC	3912
Db	3856	AATAGACTGAAGCTTGCCCTTGAGAGAGAGAAAGCTGCTGTGACAGCTATAGAGAAAGCC	3915
Oy	3913	CTTAGAAGAACCGGCATCGAGCTCCGGTCCGCCCGGGAGGAAGCTGACCAACCGAAAGCA	3972
Db	3916	CTTAGAAGAACCGGCATCGAGCTCCGGTCCGCCCGGGAGGAAGCTGACCAACCGAAAGCA	3975
Oy	3973	ACGAGCACACCAACACCCATCCACGCGCCAGCACCGCGAGGACAGATCGCATGTCCGCC	4032
Db	3976	ACGAGCACACCAACACCCATCCACGCGCCAGCACCGCGAGGACAGATGTGCCATGTCCGCC	4035
Oy	4033	ATCGTGCAGTGCAGAGACCAACCCAGTGCATGAGCTGTGCGCCCGCATCCAGC	4092
Db	4036	ATCGTGCAGTGCAGAGACCAACCCAGTGCATGAGCTGTGCGCCCGCATCCAGC	4095
Oy	4093	CGCAGAAAGAGTCTTCACTCCGAGAGAAATTAATGTCGGGCTCTTAAGSAAACGATCGAC	4152
Db	4096	CGCAGAAAGAGTCTTCACTCCGAGAGAAATTAATGTCGGGCTCTTAAGSAAACGATCGAC	4155
Oy	4153	CACAAATATTCCTCAACCGATTCAAAGTAGAGCTGAACATGCGAGCCACAAAATGTGCTGTG	4212
Db	4156	CACAAATATTCCTCAACCGATTCAAAGTAGAGCTGAACATGCGAGCCACAAAATGTGCTGTG	4215
Oy	4213	TGTCGTGATACCGTGCACCTTTGACCGCCAGGCATCCAAATGTCTGAAATGTCAGGTATG	4272
Db	4216	TGTCGTGATACCGTGCACCTTTGACCGCCAGGCATCCAAATGTCTGAAATGTCAGGTATG	4275
Oy	4273	TGTCAACCCCAAGTGTCTCAAGTGTTCGCGAGCCACTGCGGCTTGCTGCTGAATTAAGCC	4332
Db	4276	TGTCAACCCCAAGTGTCTCAAGTGTTCGCGAGCCACTGCGGCTTGCTGCTGAATTAAGCC	4335
Oy	4333	ACACACTTCACCGAGGCTTCTGCGCTGACAAAATGAAATCCCAAGGTCTTCACAGACCAAG	4392
Db	4336	ACACACTTCACCGAGGCTTCTGCGCTGACAAAATGAAATCCCAAGGTCTTCACAGACCAAG	4395
Oy	4393	GAGCCAGCAGCAGCTTGACCTTGAGAGGGTGAATGAAGTGTCCAGAGATTAACAAACGA	4452
Db	4396	GAGCCAGCAGCAGCTTGACCTTGAGAGGGTGAATGAAGTGTCCAGAGATTAACAAACGA	4455
Oy	4453	GGAACGACAGGCTTGAGACAGGAAGTACATTTGCTCGAGGGATTAATAAGTCTCATTTAT	4512
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QY	5443	CTGTTTGACCCACTTCACTCACTCGAAGTAAATTGAGATCCAGGACGCTCCTCAGCA	5502
Db	5586	CTGTTTGTGACCCACTTCACTCACTCGAAGTAAATTGAGATCCAGGACGCTCCTCAGCA	5655
QY	5503	GGGACCCCTGCGCCGAGCGTACTTGAGATCCGGAACCGCGCTACTCTGCGCCCTGCAATT	5562
Db	5656	GGGACCCCTGCGCCGAGCGTACTTGAGATCCGGAACCGCGCGTACTCTGCGCCCTGCAATT	5715
QY	5563	TTCCTCAGAGGAGTATTACTTGCGCGTCTCTCATCCAGATTAATTAAAGGTCATTGTGCTGC	5622
Db	5716	TTCCTCAGAGGAGTATTACTTGCGCGTCTCTCATCCAGATTAATTAAAGGTCATTGTGCTGC	5775
QY	5623	AAGGGAACCTCTGTGAAGAGATCCGAGCACTTGAAACACACCGGCGGCGCTGCCACTTCGCGC	5682
Db	5776	AAGGGAACCTCTGTGAAGAGATCCGAGCACTTGAAACACACCGGCGGCGCTGCCACTTCGCGC	5835
QY	5683	AG 5684	
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Job time : 3118.26 secs

Job time : 3118.26 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2005, 16:13:43 ; Search time 3286.74 Seconds
(Without alignments)
11868.626 Million cell updates/sec

Title: US-10-017-216-1

Perfect score: 6574
Sequence: 1 agagccgccagtcgggagatg.....accgagatgtagctttaga 6574

Scoring table: IDENTIFY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6574	100.0	6574	13	US-10-017-216-1
2	6574	100.0	6574	16	US-10-325-430-10
3	6574	100.0	6574	18	US-10-757-262-51
4	6162	93.7	6162	16	US-10-325-430-11
5	6159	93.7	6159	13	US-10-017-216-3
6	5684.4	86.2	5684	17	US-10-415-011-43
7	5669.8	86.2	5669	18	US-10-618-941-1
8	5661.4	86.1	5661	13	US-10-028-946-1
9	5661.4	86.1	5661	18	US-10-791-666-1
10	5631	85.7	6189	11	US-09-964-956-10
11	5631	85.7	6189	17	US-10-262-511-1

12	5629.8	85.6	6201	11	US-09-964-956-8	Sequence 8, Appl1
13	5629.8	85.6	6201	17	US-10-262-511-13	Sequence 13, Appl1
14	5358	81.5	5877	13	US-10-028-946-3	Sequence 3, Appl1
15	5358	81.5	5877	18	US-10-791-666-3	Sequence 3, Appl1
16	2575.2	39.2	2896	18	US-10-357-930-30150	Sequence 137, App
17	2564.8	39.0	3131	17	US-10-276-774-137	Sequence 7, Appl1
18	2414	36.7	2542	17	US-10-262-511-5	Sequence 5, Appl1
19	2317.2	35.2	2497	17	US-10-262-511-3	Sequence 3, Appl1
20	1841.2	28.0	1870	17	US-10-262-511-9	Sequence 9, Appl1
21	1524.2	23.2	1570	17	US-10-262-511-11	Sequence 11, Appl1
22	1467.6	22.3	1915	17	US-10-311-034-33	Sequence 33, Appl1
23	1406.4	21.4	2066	17	US-10-311-034-33	Sequence 1, Appl1
24	1397.8	21.3	1515	9	US-09-804-471A-1	Sequence 1, Appl1
25	1397.8	21.3	1515	14	US-10-238-709-1	Sequence 1, Appl1
26	1397.8	21.3	1515	17	US-10-724-554-1	Sequence 419, App
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29	768	11.7	1133	14	US-10-282-048-1	Sequence 1, Appl1
30	701.4	10.7	995	17	US-10-357-930-15814	Sequence 255, App
31	443.4	6.7	446	18	US-10-357-930-15814	Sequence 15814, A
32	436	6.6	485	18	US-10-357-930-45643	Sequence 45643, A
33	421.4	6.4	2870	17	US-10-425-114-26241	Sequence 26241, A
34	350.4	5.3	354	13	US-10-040-739-9	Sequence 9, Appl1
35	308	4.7	308	9	US-09-998-598-2328	Sequence 2328, App
36	306.4	4.7	308	9	US-09-998-598-1929	Sequence 1929, App
37	306.4	4.7	308	17	US-10-097-105-132	Sequence 132, App
38	306.4	4.7	297	9	US-09-796-692-3885	Sequence 3885, App
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41	296	4.5	297	17	US-10-154-884B-3885	Sequence 3885, App
42	296	4.5	297	18	US-10-764-324-3885	Sequence 513, App
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ALIGNMENTS

RESULT 1					
US-10-017-216-1					
; Sequence 1, Application US//10017216					
; Publication No. US20020160483A1					
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; APPLICANT: KAPLEBER, LIBERMAN, Rosana					
; TITLE OF INVENTION: 13245, A No. US20020160483A1e1 Human Myotonic Dystrophy Type Prot					
; FILE REFERENCE: 10147-57U1					
; CURRENT APPLICATION NUMBER: US/10/017,216					
; CURRENT FILING DATE: 2001-10-23					
; PRIOR APPLICATION NUMBER: US 60/242,429					
; PRIOR FILING DATE: 2000-10-23					
; NUMBER OF SEQ ID NOS: 7					
; SOFTWARE: Patentin Ver. 2.1					
; SEQ ID NO 1					
; LENGTH: 6574					
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; ORGANISM: Homo sapiens					
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Qy 5101 CTCAGCAATATCTGATCCGGAAGAGATGAGACCTGAGACCTGAGCCTGTATTCAC 5160
Db 5101 CTCAGCAATATCTGATCCGGAAGAGATGAGACCTGAGACCTGAGCCTGTATTCAC 5160
Qy 5161 TTGACCAATTCAGTATCTCATTTGGAACCAATAATTCAGAAATGACATGAAAGCAG 5220
Db 5161 TTGACCAATTCAGTATCTCATTTGGAACCAATAATTCAGAAATGACATGAAAGCAG 5220
Qy 5221 TACAGGCTCGAGGATTTCTGATTAAGATGACATTCCTTGGCACTGTGTGTTGCC 5280
Db 5221 TACAGGCTCGAGGATTTCTGATTAAGATGACATTCCTTGGCACTGTGTGTTGCC 5280
Qy 5281 GCTCTTCCAAAGCTCCCTGTCTCAATCGGAGGTGAAACAGGCGAGGAGGAGAG 5340
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Qy 5341 GAGTACTGTGTGTTTCCAGAAATTTGAGGTGTCGAGATTCTTTAGGAAGAGTAC 5400
Db 5341 GAGTACTGTGTGTTTCCAGAAATTTGAGGTGTCGAGATTCTTTAGGAAGAGTAC 5400
Qy 5401 CGCACAGAGATCTGAAGTGAAGTGGCTTACCTTTGGCTTACAGAGAACCTCAT 5460
Db 5401 CGCACAGAGATCTGAAGTGAAGTGGCTTACCTTTGGCTTACAGAGAACCTCAT 5460
Qy 5461 CTGTTTGTGACCACTTCACTCATCGAAGTAAATGATCCAGGCAAGCTCCAGCA 5520
Db 5461 CTGTTTGTGACCACTTCACTCATCGAAGTAAATGATCCAGGCAAGCTCCAGCA 5520
Qy 5521 GGGAGCCCTGCGCGAGCTACTGGAATCCGGAACCCGCGTACTGAGGCTGTCATT 5580
Db 5521 GGGAGCCCTGCGCGAGCTACTGGAATCCGGAACCCGCGTACTGAGGCTGTCATT 5580
Qy 5581 TCCTCAGGAGGATTTAGTGGCGTCCATACAGATAAATTAAGGTCAATTTGCTGC 5640
Db 5581 TCCTCAGGAGGATTTAGTGGCGTCCATACAGATAAATTAAGGTCAATTTGCTGC 5640

Db 5581 TCCTCAGGAGGATTTAGTGGCGTCCATACAGATAAATTAAGGTCAATTTGCTGC 5640
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Db 5641 AAGGAAAACCTGTGTAAGAGTCCGCACTGAACACACCGGGGCGCTCCACTCCGC 5700
Qy 5701 AGCAGCCCAACAGAGGCGCCACCACTGACAGAGACATCAAGGCGGTGCC 5760
Db 5701 AGCAGCCCAACAGAGGCGCCACCACTGACAGAGACATCAAGGCGGTGCC 5760
Qy 5761 TCCAGCCAGGCGCGCCGAGAGGCGCCAGCCAGCCGAGAGCCAGAGCAACCCACGC 5820
Db 5761 TCCAGCCAGGCGCGCCGAGAGGCGCCAGCCAGCCGAGAGCCAGAGCAACCCACGC 5820
Qy 5821 TACCGGAGGCGGACCGAGCTGCGAGGACAAAGTCTCTGCGCGCCCTGAGGCA 5880
Db 5821 TACCGGAGGCGGACCGAGCTGCGAGGACAAAGTCTCTGCGCGCCCTGAGGCA 5880
Qy 5881 GAGAAATCCCGCGCGGATGCTACAGCACTGAGAGAGCGGTCCCGGAGGCTGTT 5940
Db 5881 GAGAAATCCCGCGCGGATGCTACAGCACTGAGAGAGCGGTCCCGGAGGCTGTT 5940
Qy 5941 GAAGACAGACAGAGGCGCGCTGCTGCGGAGCGGTGAGGACCCGCTGCCAGGTG 6000
Db 5941 GAAGACAGACAGAGGCGCGCTGCTGCGGAGCGGTGAGGACCCGCTGCCAGGTG 6000
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Db 6001 AACAGGGAAGAGGAGGCTGCTTCAAGTTTACGTTAACCTGTCACTATAT 6060
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Db 6061 GACTGGAATTAAGAGCTGGAACACCTGCGAGCTAATGCTGAGAGTATCCAG 6120
Qy 6121 CTGAATGGAAGAAATCCGAGCAGAGTGAAGTCTGTCTGAGAACAGATTATGCTGA 6180
Db 6121 CTGAATGGAAGAAATCCGAGCAGAGTGAAGTCTGTCTGAGAACAGATTATGCTGA 6180
Qy 6181 GCAAGTTCATGTATCTTACAGCTGTGATCTTAAATAATGCGCTTAAGCTGCAAGC 6240
Db 6181 GCAAGTTCATGTATCTTACAGCTGTGATCTTAAATAATGCGCTTAAGCTGCAAGC 6240
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Qy 6301 AACCTCATTAAGAAATGAGAAAGCTTAAATTTCTATAGAAATGACACTCCGAGGC 6360
Db 6301 AACCTCATTAAGAAATGAGAAAGCTTAAATTTCTATAGAAATGACACTCCGAGGC 6360
Qy 6361 GAGAGCAATCTGTGTTTGAATTTTGAAGACAGGCAAGCAACATGATTTAGTTCCA 6420
Db 6361 GAGAGCAATCTGTGTTTGAATTTTGAAGACAGGCAAGCAACATGATTTAGTTCCA 6420
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RESULT 2
US-10-325-430-10
; Sequence 10, Application US/10325430
; Publication No. US2003015325A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc

APPLICANT: Siles-Santiago, Immaculada
APPLICANT: Rosenfeld, Julie Beth
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
TITLE OF INVENTION: 32838, 336 and 52908
FILE REFERENCE: MP101-294PIRM
CURRENT APPLICATION NUMBER: US/10/325,430
PRIOR FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/341,953
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 6574
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-325-430-10

Query Match 100.0%; Score 6574; DB 16; Length 6574;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGAGCCGCGAGTGGGGAGATGTTGAAATCAATAATGAGCGCGAATCCTTGGATGCT 60
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DB 61 GGTGCTGCTGAACCCATTTGCGACCGGGCTCCAGCTGATTTGTTCTTCCAGGGAAA 120
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DB 181 CTCTTGTCTCTTTGAGAAATGCACTGACCTGCTCTGATGAAATTAAGACGTGAC 240
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DB 241 AACTTGTCCGGAAGTATCCGACACATAGCTGATTAAGAGCTCCAGCTTGGCA 300
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DB 301 AAGGACTTGAAGTCAAGAGCTTGTAGGTTGTGTCACCTTGTGAAGTCAAGGCTTGGCA 360
QY 361 AAGAGAAAGCAACCGGGACATCTATGCTATGAAAGTGAAGAAAGCTTTATG 420
DB 361 AAGAGAAAGCAACCGGGACATCTATGCTATGAAAGTGAAGAAAGCTTTATG 420
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DB 421 GCCCAGAGAGAGTTCATTTTGAAGAAAGCGGAACATATTATCTGAAACACAAAC 480
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DB 481 CCGTGGATCCCAATTACAGATGCTTTCAGGAGAAATACCTTATCTGATGAG 540
QY 541 GAATATCAGCTGAGAGGAGCTTGTCTGATCTTTGAATATGATGAGACAGTTAGAT 600
DB 541 GAATATCAGCTGAGAGGAGCTTGTCTGATCTTTGAATATGATGAGACAGTTAGAT 600
QY 601 GAAATCTGATACAGTTTACCTAGCTGAGCTGATTTGCTGTTCAACGCTTCACTG 660
DB 601 GAAATCTGATACAGTTTACCTAGCTGAGCTGATTTGCTGTTCAACGCTTCACTG 660
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DB 661 ATGGATAGTGTGATGAGATCAAGCTGAGAGACATTCGTGTGACCGACAGACAC 720
QY 721 ATCAAGCTGTGATTTGGATCTGCCGGAATAATGATTCAAACAAAGATGGATGCC 780
DB 721 ATCAAGCTGTGATTTGGATCTGCCGGAATAATGATTCAAACAAAGATGGATGCC 780

QY 781 AAATCCCGATTGGAGCCCGAGATTACATGCTCCGAGAGTGTGATGAGACGGG 840
DB 781 AAATCCCGATTGGAGCCCGAGATTACATGCTCCGAGAGTGTGATGAGACGGG 840
QY 841 GATGAGAAAGGACCTAGCGCTGAGCTGTGATGATGAGGAGGCTGATTTGCTAT 900
DB 841 GATGAGAAAGGACCTAGCGCTGAGCTGTGATGATGAGGAGGCTGATTTGCTAT 900
QY 901 GATGATTTATGAGAGATCCCTTCCGAGAGGAACTTCCGAACTTCAATAC 960
DB 901 GATGATTTATGAGAGATCCCTTCCGAGAGGAACTTCCGAACTTCAATAC 960
QY 961 ATTATGAATTCAGAGGTTTGAATTTCCAGATGACCCCAAGTGGAGATGACTT 1020
DB 961 ATTATGAATTCAGAGGTTTGAATTTCCAGATGACCCCAAGTGGAGATGACTT 1020
QY 1021 CTGTGATCTGATTCAAAGCTTGTGTGCGGCGAGAAAGAGAGCTGAAAGTCTT 1080
DB 1021 CTGTGATCTGATTCAAAGCTTGTGTGCGGCGAGAAAGAGAGCTGAAAGTCTT 1080
QY 1081 TGTGCTCATCTTTCTTCTTAAATGATCTGGAACACATTTGTAATCTCTCCGCC 1140
DB 1081 TGTGCTCATCTTTCTTCTTAAATGATCTGGAACACATTTGTAATCTCTCCGCC 1140
QY 1141 TTGCTCCGACCTCAAGCTGAGATGACCTCCAAATTTGATGAAACAGAGAAAT 1200
DB 1141 TTGCTCCGACCTCAAGCTGAGATGACCTCCAAATTTGATGAAACAGAGAAAT 1200
QY 1201 TGTGAGTTTCAATCTCTCTGTCAGAGCTGAGACCTTCCAGGCTTCTGAGTAAAG 1260
DB 1201 TGTGAGTTTCAATCTCTCTGTCAGAGCTGAGACCTTCCAGGCTTCTGAGTAAAG 1260
QY 1261 CCGTTTGTGGGTTTCTGACAGCAAGCACTGGGATTTCTGTGATGATGATGTT 1320
DB 1261 CCGTTTGTGGGTTTCTGACAGCAAGCACTGGGATTTCTGTGATGATGATGTT 1320
QY 1321 GGTGAGGCTGAGACCTCCCTGCAAGACTAGCTCCATGAAAGAACTTCTCATCAA 1380
DB 1321 GGTGAGGCTGAGACCTCCCTGCAAGACTAGCTCCATGAAAGAACTTCTCATCAA 1380
QY 1381 ACCAAAGAGCTCAAGACTCTGAGCAAGTCTCAAGATGAGAGAGAAATGACCCGG 1440
DB 1381 ACCAAAGAGCTCAAGACTCTGAGCAAGTCTCAAGATGAGAGAGAAATGACCCGG 1440
QY 1441 TTACATCGAGAGTGTGAGAGTGTGCTGTGATGATGAGAGAGTGTGAGTGAAG 1500
DB 1441 TTACATCGAGAGTGTGAGAGTGTGCTGTGATGATGAGAGAGTGTGAGTGAAG 1500
QY 1501 GCTCTGAGACTCAAGATCCCTCTGAGAGAGAGCTTGTCACTCAACAGATATC 1560
DB 1501 GCTCTGAGACTCAAGATCCCTCTGAGAGAGAGCTTGTCACTCAACAGATATC 1560
QY 1561 AGTAGCTTAAAGCAATTTGAGAGAGAGAGAGTGTCCAGAGAGATGACAA 1620
DB 1561 AGTAGCTTAAAGCAATTTGAGAGAGAGAGAGTGTCCAGAGAGATGACAA 1620
QY 1621 GCACTGAGCTTCTCATGATATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1621 GCACTGAGCTTCTCATGATATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
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DB 1681 CAGAGATCAGAGCTCAAGTGTGAAGAAATGAGAGTGTGAAGAGAGAGAT 1740
QY 1741 CTGTGCTCAGCAAGAGAGAGATCTCTAGATCTGAGCTGAGAGAGTCTGGCTT 1800
DB 1741 CTGTGCTCAGCAAGAGAGAGATCTCTAGATCTGAGCTGAGAGAGTCTGGCTT 1800
QY 1801 GCTGCTGAAGAAATTCAGAGAGAGAGAGAGAGATGATGATGATGATGATGATG 1860
DB 1801 GCTGCTGAAGAAATTCAGAGAGAGAGAGAGAGATGATGATGATGATGATGATG 1860

QY	1861	GATTCAGGGAGACCTGGAAGTGGAGAAATATGCGAACTGGAGAGATCAATGCTGACAG	1920
Db	1861	GATCAGGGAGACCTGGAAGTGGAGAAATATGCGAACTGGAGAGATCAATGCTGACAG	1920
QY	1921	CAGCTCAAAATTCAGAGACTCCAGAGAAACTGGAGAGGCTGCAGAAAGACGAGCCGAG	1980
Db	1921	CAGCTCAAAATTCAGAGACTCCAGAGAAACTGGAGAGGCTGCAGAAAGACGAGCCGAG	1980
QY	1981	AGGGAGCTGGAGAGCTGCAGAACCGAGAGGATTTCTTGAAGGCATCAGAAAGACTG	2040
Db	1981	AGGGAGCTGGAGAGACTGCAGAACCGAGAGGATTTCTTGAAGGCATCAGAAAGACTG	2040
QY	2041	GTGGAAGCTGGAGAACGCCGCCATTTCTTGGAGAACAGGTAAGAGACTAGAGACATG	2100
Db	2041	GTGGAAGCTGGAGAACGCCGCCATTTCTTGGAGAACAGGTAAGAGACTAGAGACATG	2100
QY	2101	GAGCTTAGAGAAAACAGACTGAGAGATGACATCCAGCAAAATCCCAACAGATCCAGCAG	2160
Db	2101	GAGCTTAGAGAAAACAGACTGAGAGATGACATCCAGCAAAATCCCAACAGATCCAGCAG	2160
QY	2161	ATGGCTGATPAAATTCCTGAGCTCGAAGAGAAAACATGGGAGGCCCCAAGTTCAGCCCAG	2220
Db	2161	ATGGCTGATPAAATTCCTGAGCTCGAAGAGAAAACATGGGAGGCCCCAAGTTCAGCCCAG	2220
QY	2221	CACCTAGAAGTGCACCTGAAAACAGAAAGCAGCACTATGAGAAAAGATTAAAGTTTG	2280
Db	2221	CACCTAGAAGTGCACCTGAAAACAGAAAGCAGCACTATGAGAAAAGATTAAAGTTTG	2280
QY	2281	GACCAATCAGATPAAAGAAAGACCTGGCTGACAAGAGACATGAGGAACATGATGACAGAG	2340
Db	2281	GACCAATCAGATPAAAGAAAGACCTGGCTGACAAGAGACATGAGGAACATGATGACAGAG	2340
QY	2341	CACGAGAGGAGGCCCATGAGAAAGGCAAAATTTCTCAGCGAAACGAAAGCGAGATCAAT	2400
Db	2341	CACGAGAGGAGGCCCATGAGAAAGGCAAAATTTCTCAGCGAAACGAAAGCGAGATCAAT	2400
QY	2401	GCTATGATTTCCAGATATCAATCCCTGGAACAGAGATTGTGAATCTGTGAAGCCAAAT	2460
Db	2401	GCTATGATTTCCAGATATCAATCCCTGGAACAGAGATTGTGAATCTGTGAAGCCAAAT	2460
QY	2461	AAACTTGGAGCAAAATPAGCAGTCTTTTAAACCAAGAGAAACATGAAGGCCCAAGAAAGATG	2520
Db	2461	AAACTTGGAGCAAAATPAGCAGTCTTTTAAACCAAGAGAAACATGAAGGCCCAAGAAAGATG	2520
QY	2521	ATTTCTGAACTCAGAGCAACAGAAATTTTAACTCTGAGACACAGGCTGGGAAGTTGAGGCC	2580
Db	2521	ATTTCTGAACTCAGAGCAACAGAAATTTTAACTCTGAGACACAGGCTGGGAAGTTGAGGCC	2580
QY	2581	CAGAACCGAAAACCTGGAGAGCAGCTGGAGAAATCGAACCAAGAACCAACATGACAAAG	2640
Db	2581	CAGAACCGAAAACCTGGAGAGCAGCTGGAGAAATCGAACCAAGAACCAACATGACAAAG	2640
QY	2641	AATCGGCTGCTGAAACTGAGACAAAGATTGCGGAGGTCAGTCTAGAGCAGAGAGCAG	2700
Db	2641	AATCGGCTGCTGAAACTGAGACAAAGATTGCGGAGGTCAGTCTAGAGCAGAGAGCAG	2700
QY	2701	AAACTGGAAGCTCAAGGCCCGACAGCTACAGACTCAAGCTCTCCCTGACAGAGGCCAGTCA	2760
Db	2701	AAACTGGAAGCTCAAGGCCCGACAGCTACAGACTCAAGCTCTCCCTGACAGAGGCCAGTCA	2760
QY	2761	CAGTTGACAGCCCTGCAAGGCTGACAGCGCGGCCCTTGGAGAGCCAGCTTCCGACAGGCCAAG	2820
Db	2761	CAGTTGACAGCCCTGCAAGGCTGACAGCGCGGCCCTTGGAGAGCCAGCTTCCGACAGGCCAAG	2820
QY	2821	ACAGAGCTTGAAGAGACCAACAGCAAGACTGGAAGAGAGATCCAGGCATCCAGGCACAT	2880
Db	2821	ACAGAGCTTGAAGAGACCAACAGCAAGACTGGAAGAGAGATCCAGGCATCCAGGCACAT	2880
QY	2881	AGAGATGAAAATCCAGCGCAAAATTTGATGCTCTTCGTAAACGCTGTACTGTAAATCAAGAC	2940
Db	2881	AGAGATGAAAATCCAGCGCAAAATTTGATGCTCTTCGTAAACGCTGTACTGTAAATCAAGAC	2940
QY	2941	CTGGAGAGACGCTPAAACCAAGCTGACCGAGAGAACGCTGAATCTCAACCAACAAATCTTC	3000

Db	2941	CTGGAGGAGCACATTAACGAGCTGACCGAGGACAACGCTGAACCTCAACAACTTTC	3000
QY	3001	TACTGTCCAAACAACCTGAGTAAGGCTCTGGCGGCAACGACGAATTGTACAACTGGCA	3066
Db	3001	TACTGTCCAAACAACCTGATBAGGCTTCTGGCGCAACGACGAATTGTACAACTGGCA	3066
QY	3061	AGTGAAGTGAGCCATCTCCGCGGAGATCAACGGAACGAGATGACACTTACCGACG	3122
Db	3061	AGTGAAGTGAGCCATCTCCGCGGAGATCAACGGAACGAGATGACACTTACCGACG	3122
QY	3121	AAGCAAAACGATGAGGCTGTAAAGCCACGTGCACATGCTGTAGAGAAACAGTCATGAT	3188
Db	3121	AAGCAAAACGATGAGGCTGTAAAGCCACGTGCACATGCTGTAGAGAAACAGTCATGAT	3188
QY	3181	TTGGAGGCGCTTAAACGATGAGCTGTAAAAAAGACGGCAGTGGAGGCGCTGGAGAGAC	3244
Db	3181	TTGGAGGCGCTTAAACGATGAGCTGTAAAAAAGACGGCAGTGGAGGCGCTGGAGAGAC	3244
QY	3241	GTCTCGGGTATGAGAAATCCCACTTTAGTGTGCGGTTTCGAGACCTGCAGAAATGCTG	3300
Db	3241	GTCTCGGGTATGAGAAATCCCACTTTAGTGTGCGGTTTCGAGACCTGCAGAAATGCTG	3300
QY	3301	GACACCGAGAAACAGAGAGGCGGAGACCGCATCAGCGGATCACCGATCTCGCAGGTC	3366
Db	3301	GACACCGAGAAACAGAGAGGCGGAGACCGCATCAGCGGATCACCGATCTCGCAGGTC	3366
QY	3361	GTGAGCTTGGCAGTGAAGAGCAACAGGCTGAGATTCCTCGCTTGCACAGGCTCTCAA	3422
Db	3361	GTGAGCTTGGCAGTGAAGAGCAACAGGCTGAGATTCCTCGCTTGCACAGGCTCTCAA	3422
QY	3421	GAGCGAAGCTGGAAGGCGGAGAGGCTCTGTACAAGCTCAATGACCTGTGAGAAAGAAAGAT	3488
Db	3421	GAGCGAAGCTGGAAGGCGGAGAGGCTCTGTACAAGCTCAATGACCTGTGAGAAAGAAAGAT	3488
QY	3481	GCTATGCTTGAATGAATGCCGAAGCTTACAGCAGAAAGCTGGAAGCTGAAACGAGAGCTC	3544
Db	3481	GCTATGCTTGAATGAATGCCGAAGCTTACAGCAGAAAGCTGGAAGCTGAAACGAGAGCTC	3544
QY	3541	AAACGAGAGGCTTCTGGAAAGACCAAGCCAAATTACGAGCAGATGAGACCTGCACAAAAAT	3600
Db	3541	AAACGAGAGGCTTCTGGAAAGACCAAGCCAAATTACGAGCAGATGAGACCTGCACAAAAAT	3600
QY	3601	CACATTTTCGCTGACTCAAGGACTGCAAGAAAGCTTGAATCGGGCTGATCTACTAG	3666
Db	3601	CACATTTTCGCTGACTCAAGGACTGCAAGAAAGCTTGAATCGGGCTGATCTACTAG	3666
QY	3661	ACAGAAAGAAATGACTTGGAGATACACTGTGAAAAACCTCAGTTCCTATTTTCATGAA	3722
Db	3661	ACAGAAAGAAATGACTTGGAGATACACTGTGAAAAACCTCAGTTCCTATTTTCATGAA	3722
QY	3721	AAGGTGAAAAATGGAAGGCACTAATTTCTCAACAAACCAACCTATTTTCTGTCTGCAAGCC	3788
Db	3721	AAGGTGAAAAATGGAAGGCACTAATTTCTCAACAAACCAACCTATTTTCTGTCTGCAAGCC	3788
QY	3781	AAAAATGGAACCACTGCTAAAAAAGAGGTTTATTAGTCGACGGAAGAGAGACCTT	3844
Db	3781	AAAAATGGAACCACTGCTAAAAAAGAGGTTTATTAGTCGACGGAAGAGAGACCTT	3844
QY	3841	GCTTTACCAACAGGTTCCCTGCACTTACAAAGAGTGAAGCTGGGCGCTGGAGAAAGAG	3900
Db	3841	GCTTTACCAACAGGTTCCCTGCACTTACAAAGAGTGAAGCTGGGCGCTGGAGAAAGAG	3900
QY	3901	AAAGCTCGCTGTGCAGAGCTAGAGGAAGCCCTTCAGAAAGACCCGATCGAGCTCCGCTCC	3966
Db	3901	AAAGCTCGCTGTGCAGAGCTAGAGGAAGCCCTTCAGAAAGACCCGATCGAGCTCCGCTCC	3966
QY	3961	GCCCGGAGAGAGGTGGCCACCCGAAAGCAACGAGCACTCAGACCCATCCATCCAGCCAGCC	4022
Db	3961	GCCCGGAGAGAGGTGGCCACCCGAAAGCAACGAGCACTCAGACCCATCCATCCAGCCAGCC	4022
QY	4021	ACCGCGAGGAGCAGATGCGCATGTCCGCATGTGTGCGCAGAGCACAGCCAGT	4080

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5041 GGGGCTGTGATCTGTGAG 5100
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6181 GAGAGATTAAG 6240
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QY 6241 CAGCCACTCTGCTTACCAAAAAAGATCTTACTATGCAACATGCTAAGAAACAACTTTGTA 6300
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Db 6301 AACCTCATCTAGAAATCGAAAGCTTCTAATTTCTATAGAAATGACACTCCCTGGAGCC 6360
QY 6361 GAGAGACAATCTGTTGTTGATTTTGAAGGACAGGCAAGACCAACTGTATTTAGTTTCA 6420
Db 6361 GAGAGACAATCTGTTGTTGATTTTGAAGGACAGGCAAGACCAACTGTATTTAGTTTCA 6420
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RESULT 3
US-10-757-262-51
/ Sequence 51, Application US/10757262
/ Publication No. US20040197825A1
/ GENERAL INFORMATION:
/ APPLICANT: Karicheti, Venkateswarlu
/ APPLICANT: Eliasof, Scott D.
/ APPLICANT: Silos-Santiago, Immaculada
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
/ TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18960, 2047,
/ TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43238, 44373, 51164,
/ TITLE OF INVENTION: 18540, 11652, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
/ TITLE OF INVENTION: 15347, 1165, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
/ TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
/ TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
/ TITLE OF INVENTION: 2243, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
/ FILE REFERENCE: MP103-007PIRNMNIM
/ CURRENT APPLICATION NUMBER: US/10/757,262
/ CURRENT FILING DATE: 2004-01-14
/ PRIOR APPLICATION NUMBER: US 60/440,318
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/444,783
/ PRIOR FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: US 60/457,901
/ PRIOR FILING DATE: 2003-03-27
/ PRIOR APPLICATION NUMBER: US 60/468,775
/ PRIOR FILING DATE: 2003-05-08
/ PRIOR APPLICATION NUMBER: US 60/471,614
/ PRIOR FILING DATE: 2003-05-19
/ PRIOR APPLICATION NUMBER: US 60/478,742
/ PRIOR FILING DATE: 2003-06-16
/ PRIOR APPLICATION NUMBER: US 60/488,529
/ PRIOR FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: US 60/491,156
/ PRIOR FILING DATE: 2003-07-30
/ PRIOR APPLICATION NUMBER: US 60/499,594
/ PRIOR FILING DATE: 2003-09-02
/ PRIOR APPLICATION NUMBER: US 60/506,332
/ PRIOR FILING DATE: 2003-09-26
/ NUMBER OF SEQ ID NOS: 136
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 51
/ LENGTH: 6574
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:

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[illegible]

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Db	1021	CTTGTATCTGATTTCAAAGCTTTGTGCGCGGCAGAAAGAGACTGAATTTGAAGTCTT	1080
Oy	1081	TGCTGCGACTCTTCTTCTCTTAAATTTGACTGGAAACAATTCTGTAACCTCTCCCCC	1140
Db	1081	TGCTGCGACTCTTCTTCTTAAATTTGACTGGAAACAATTCTGTAACCTCTCCCCC	1140
Oy	1141	TTTCGTTTCCCACTTCAGTCTTGACGATGACACTTTCCAATTTTGTATGAACCGAAGAAAT	1200
Db	1141	TTTCGTTTCCCACTTCAGTCTTGACGATGACACTTTCCAATTTTGTATGAACCGAAGAAAT	1200
Oy	1201	TCGTGAGGTTTTATCTCTCCGTGCGAGCTGAGCCCCCTAGGCTTCTCGGGTGAAGAACTG	1260
Db	1201	TCGTGAGGTTTTATCTCTCCGTGCGAGCTGAGCCCCCTAGGCTTCTCGGGTGAAGAACTG	1260
Oy	1261	CCGTTTGTGTGGGTTTTCTGTACAGCAAGGCACTGGGGATTTCTTGTGATCTTGAGTCTGTT	1320
Db	1261	CCGTTTGTGTGGGTTTTCTGTACAGCAAGGCACTGGGGATTTCTTGTGATCTTGAGTCTGTT	1320
Oy	1321	GTGTGCGGTTCTGGAAGTCTCCCTGCGCCAGACTGACTTCACATGAGAAAGAACTTCTATCAA	1380
Db	1321	GTGTGCGGTTCTGGAAGTCTCCCTGCGCCAGACTGACTTCACATGAGAAAGAACTTCTATCAA	1380
Oy	1381	AGCAAAGAGCTACAAAGACTCTCAGGACAAAGTGTACAACAATGAGGACGAGAAATGACCCGG	1440
Db	1381	AGCAAAGAGCTACAAAGACTCTCAGGACAAAGTGTACAACAATGAGGACGAGAAATGACCCGG	1440
Oy	1441	TTTATCATCGGAGAGTGTCAAGAGTGAAGCTGTGCTTAAGTCAGAAAGAGTGTGAAGCTGAA	1500
Db	1441	TTTATCATCGGAGAGTGTCAAGAGTGAAGCTGTGCTTAAGTCAGAAAGAGTGTGAAGCTGAA	1500
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Db	1501	GCTCTGTGAGACTCAGAGATCCCTCTCTGAGACAGAACTTGTCTTACCTTACATCACAGAAATGC	1560
Oy	1561	AGTAGGCTTAAAGCCGAAGTTTGGACCAAGCAAGGATGAGGTGTCCCGAGAGATGACAAA	1620
Db	1561	AGTAGGCTTAAAGCCGAAGTTTGGACCAAGCAAGGATGAGGTGTCCCGAGAGATGACAAA	1620
Oy	1621	GCACTGCAAGTCTTCCATGATATCAGAGACGAGCCCGAAGCTTCCAAGAAATCAAAGAG	1680
Db	1621	GCACTGCAAGTCTTCCATGATATCAGAGACGAGCCCGAAGCTTCCAAGAAATCAAAGAG	1680
Oy	1681	CAGAGATACAGAGCTCAAAGTGAAGAAATGAGTTGATGATGAATCAAGTTGGAAGAGAT	1740
Db	1681	CAGAGATACAGAGCTCAAAGTGAAGAAATGAGTTGATGATGAATCAAGTTGGAAGAGAT	1740
Oy	1741	CTTGTCTTCAGAAABAAGCCGAGGTGATCTTACCAATTTGAGCTGAGAGACTCTCGGCTT	1800
Db	1741	CTTGTCTTCAGAAABAAGCCGAGGTGATCTTACCAATTTGAGCTGAGAGACTCTCGGCTT	1800
Oy	1801	GCTGCTGAAGAATTTCAAGCCGGAAGACGACAGATGTGAGCATTAACCTTTGAAGGCTTAAG	1860
Db	1801	GCTGCTGAAGAATTTCAAGCCGGAAGACGACAGATGTGAGCATTAACCTTTGAAGGCTTAAG	1860
Oy	1861	GATCAAGGGAAGCCTTGAAGTGGAGAAATATGCGAAACTGGAAGATCAATGCTGAGACG	1920
Db	1861	GATCAAGGGAAGCCTTGAAGTGGAGAAATATGCGAAACTGGAAGATCAATGCTGAGACG	1920
Oy	1921	CAGCTCAAAATTTCCAGAGCTCCAAGAGAAATCTGAGAAAGGCTGTCAAAAGGACCGAGC	1980
Db	1921	CAGCTCAAAATTTCCAGAGCTCCAAGAGAAATCTGAGAAAGGCTGTCAAAAGGACCGAGC	1980
Oy	1981	AGGAGAGCTGAGAAAGCTGCAGAACCGAAGAGATTTCTTGAAGGATCAGAAAGAAAGCTG	2040
Db	1981	AGGAGAGCTGAGAAAGCTGCAGAACCGAAGAGATTTCTTGAAGGATCAGAAAGAAAGCTG	2040
Oy	2041	GTGGAAAGCTGAGAAAGCCGCGCATTTCTTGTGAGAACCAAGTAAAGAGACTGAGACCAATG	2100

Db	2041	GTGGAGCTGAGAAACGCCCCATTCTCTGGAGAACAAAGTAAAGAGACTAGAACCATG	2100
QY	2101	GAGGCTAGAGAAAACAGACTGAGAGATGACATCCAGACAAATATCCACAGATCCAGCAG	2160
Db	2101	GAGGCTAGAGAAAACAGCTGAGAGATGACATCCAGACAAATATCCACAGATCCAGCAG	2160
QY	2161	ATGCTGCTAAATTTCTGGAGCTCGAAGAGAAACATGGGAGGCCCAAGTCTCAGCCAG	2220
Db	2161	ATGCTGCTAAATTTCTGGAGCTCGAAGAGAAACATGGGAGGCCCAAGTCTCAGCCAG	2220
QY	2221	CACCTAGAGTGCACCTGAAACAAAGAGAGAGACTATGAGAGAAAGATTAAAGTGTG	2280
Db	2221	CACCTAGAGTGCACCTGAAACAAAGAGAGAGACTATGAGAGAAAGATTAAAGTGTG	2280
QY	2281	GACAAATCAGATPAAAGAAAGACTGGCTGACAAAGAGACACTGGAGAACTATGTCAGAGA	2340
Db	2281	GACAAATCAGATPAAAGAAAGACTGGCTGACAAAGAGACACTGGAGAACTATGTCAGAGA	2340
QY	2341	CACGAGAGAGGCCCCATGAGAGGCGCAAAATTTCTCAGCGAACAGAGGCGATATCAAT	2400
Db	2341	CACGAGAGAGGCCCCATGAGAGGCGCAAAATTTCTCAGCGAACAGAGGCGATATCAAT	2400
QY	2401	GCTATGATTTCCAGATCAAGTCCCTGGAACAGAGATTGGGAATGTCCTGAAGCCAT	2460
Db	2401	GCTATGATTTCCAGATCAAGTCCCTGGAACAGAGATTGGGAATGTCCTGAAGCCAT	2460
QY	2461	AAACTTGCAGCAATATAGAGTCTTTTAAACCAAGAAACATGAAAGGCCCAAGAGAGATG	2520
Db	2461	AAACTTGCAGCAATATAGAGTCTTTTAAACCAAGAAACATGAAAGGCCCAAGAGAGATG	2520
QY	2521	ATTTCTGAATCAGGCAACAGAAATTTTAACTTGGAGACACAGGCTGGGAAGTTGAGGCGC	2580
Db	2521	ATTTCTGAATCAGGCAACAGAAATTTTAACTTGGAGACACAGGCTGGGAAGTTGAGGCGC	2580
QY	2581	CAGAACCGAAAACTGGAGAGACAGCTGAGAGAAATCAAGCCACCAAGACCAAGTGAACAG	2640
Db	2581	CAGAACCGAAAACTGGAGAGACAGCTGAGAGAAATCAAGCCACCAAGACCAAGTGAACAG	2640
QY	2641	AAATGGGCTGCTGGAACCTGGAGACAAAGATTGGGGAGGCTCAGTCTAGAGACAGAGAGCAG	2700
Db	2641	AAATGGGCTGCTGGAACCTGGAGACAAAGATTGGGGAGGCTCAGTCTAGAGACAGAGAGCAG	2700
QY	2701	AAACTGAGCTCAAGCGCCAGCTACAGAGCTACAGCTCTCCCTGCAAGAGCGCGAGTCA	2760
Db	2701	AAACTGAGCTCAAGCGCCAGCTACAGAGCTACAGCTCTCCCTGCAAGAGCGCGAGTCA	2760
QY	2761	CAGTTGACAGCCCTGACAGGCTGACCGGCGGCCCTTGGAGAGCCAGCTTCCGACGCCAG	2820
Db	2761	CAGTTGACAGCCCTGACAGGCTGACCGGCGGCCCTTGGAGAGCCAGCTTCCGACGCCAG	2820
QY	2821	ACAGAGCTGGAAGAGACCAACAGAGAAAGCTGAAGAGATCCAGGCACTCAGGCGCAT	2880
Db	2821	ACAGAGCTGGAAGAGACCAACAGAGAAAGCTGAAGAGATCCAGGCACTCAGGCGCAT	2880
QY	2881	AGAGATGAAATCCAGCGCCAAATTTGATGCTCTTCTGTAACAGCTGTACTGTATACAGAC	2940
Db	2881	AGAGATGAAATCCAGCGCCAAATTTGATGCTCTTCTGTAACAGCTGTACTGTATACAGAC	2940
QY	2941	CTGAGAGAGACGCTPAAACAGCTGACCGAGAGACACGCTGAATCTCAACACCAAACTTC	3000
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QY	3001	TACTTGTCCAAACAACTCGAATGAGGCTTCTGGGCGCCAAACGAGATTTGTAACAATCGGA	3060
Db	3001	TACTTGTCCAAACAACTCGAATGAGGCTTCTGGGCGCCAAACGAGATTTGTAACAATCGGA	3060
QY	3061	AGTGAAGTGAACCATCTCCGCGGAGATCAACGAAACGAGATGCACTTAAACCAAGCCAG	3120
Db	3061	AGTGAAGTGAACCATCTCCGCGGAGATCAACGAAACGAGATGCACTTAAACCAAGCCAG	3120
QY	3121	AAGCAAAAGATGAGGCTCTGGAAGACACGCTGACCAATGCTGGAGAAACAGGTCATGGAT	3180
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QY 3241 GTCCCTGGGTATGAGAAATCCAGTTTGAAGTGTGAGGTTGAGAGAGCTGAGAGAAATGCTG 3300
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Db 3301 GACACCGAAGAAAGAGACAGAGCGGCGAGGCGGATCAGCGGATCAACGAGTCTGCGCAGAGT 3360
QY 3361 GTGAGAGCTGACAGAAAGAGCAAGGCGTGAATTTCTGCTGTGACAGAGGCTCTCAAA 3420
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QY 3421 GAGCAGAGAGCTGAAGGCGGAGAGCTCTCTGACAGAGCTCAATGACCTGAGAGAGAGCAT 3480
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Qy 6361 GAGAGCAATCTGTTGTGATTTTGAAGACAGGCAAGACCAACATGATTTAGTTTCA 6420
Db 6361 GAGAGCAATCTGTTGTGATTTTGAAGACAGGCAAGACCAACATGATTTAGTTTCA 6420
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Db 6481 ATGTGAGGCTCAGTCCCTGTTTCCAGAAATTTTACTGGCAAGAGTTAGATTCAATT 6540
Qy 6541 TTGGCTTAAGAAAAATCGAAGATGTAGTTTGA 6574
Db 6541 TTGGCTTAAGAAAAATCGAAGATGTAGTTTGA 6574

RESULT 4
US-10-325-430-11
; Sequence 11, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Siles-Santiago, Immaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; FILE REFERENCE: MP101-294PIRM
; CURRENT APPLICATION NUMBER: US/10/325,430
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6162
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6162)
US-10-325-430-11

Query Match 93.7%; Score 6162; DB 16; Length 6162;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ATGTGAATTCATTAATATGAGAGCGGAGTCCCTTGGAGTGTGCTGTAACCAT 78
Db 1 ATGTGAATTCATTAATATGAGAGCGGAGTCCCTTGGAGTGTGCTGTAACCAT 60
Qy 79 GCCAGCCGCGCTCCAGGCTGATCTGTTTCCAGGAGAAACCACTTTATGACTCA 138
Db 61 GCCAGCCGCGCTCCAGGCTGATCTGTTTCCAGGAGAAACCACTTTATGACTCA 120
Qy 139 CAGCAGATCTCTCTTTTCCGAGAGGATTTAGTCCCTTTGTTCTTTTGA 198
Db 121 CAGCAGATCTCTCTTTTCCGAGAGGATTTAGTCCCTTTGTTCTTTTGA 180
Qy 199 GAATGAGTCACTGCTGCTGATGAAGATTAAGACGTGAGCACTTTGTCCGAGAT 258
Db 181 GAATGAGTCACTGCTGCTGATGAAGATTAAGACGTGAGCACTTTGTCCGAGAT 240
Qy 259 TCCGACCATAGTGAATTAAGAGTCCAGCTTCCGCAAGGACTTCAAGTCA 318
Db 241 TCCGACCATAGTGAATTAAGAGTCCAGCTTCCGCAAGGACTTCAAGTCA 300
Qy 319 AGCTTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 378
Db 301 AGCTTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 360
Qy 379 GACATATGCTATGAAAGTATGAAGAGGCTTTTATGAGGAGGAGGTTTCA 438
Db 361 GACATATGCTATGAAAGTATGAAGAGGCTTTTATGAGGAGGAGGTTTCA 420
Qy 439 TTTTGAAGAGAGGAGCAATATATCTGAGACCAAGCCGTTGATCCCAATTA 498
Db 421 TTTTGAAGAGAGGAGCAATATATCTGAGACCAAGCCGTTGATCCCAATTA 480

QY	499	CAGTATGCTTTTCAAGACAAATAATCACTTATCTGTATGAGAAATATACGCTGAGAGG	558
Db	481	CAGTATGCTTTTCAAGACAAATAATCACTTATCTGTATGAGAAATATACGCTGAGAGG	540
QY	559	GACTTCGTGCATCTTTTGAATTAATATGAGACACAGTTATATGAAAACTGATATCACTTT	618
Db	541	GACTTCGTGCATCTTTTGAATTAATATGAGACACAGTTATATGAAAACTGATATCACTTT	600
QY	619	TACCTAGCTGAGCTGATTTTGTGCTGTTCACAGCGTTCACTGTAGTGGATACGTGATCCGA	678
Db	601	TACCTAGCTGAGCTGATTTTGTGCTGTTCACAGCGTTCACTGTAGTGGATATCGTGCATCCGA	660
QY	679	GACATCAAGCTGAGAAACATTCCTGTTGACCCGACACGACACATCAAGCTGTGATATTTT	738
Db	661	GACATCAAGCTGAGAAACATTCCTGTTGACCCGACACGACACATCAAGCTGTGATATTTT	720
QY	739	GGATCTGCCGCGAAAAATGAAATTCAAACAAGATGTAATGSCAAATCCCGATTTGGAGACC	798
Db	721	GGATCTGCCGCGAAAAATGAAATTCAAACAAGATGTAATGSCAAATCCCGATTTGGAGACC	780
QY	799	CCAGATTAATATGAGCTCTCTGAATGTCTGACTGTGATGAAAGGGGATGAAAGGCACCTAC	858
Db	781	CCAGATTAATATGAGCTCTCTGAATGTCTGACTGTGATGAAAGGGGATGAAAGGCACCTAC	840
QY	859	GGCCTTGACCTGTGACTGTGTGTCAAGTGGGCGGTGATTGCCATATGATATGATTTATGGGAGA	918
Db	841	GGCCTTGACCTGTGACTGTGTGTCAAGTGGGCGGTGATTGCCATATGATATGATTTATGGGAGA	900
QY	919	TCCCTCTTGGCAGAGGGAACTTCTGCGAAGACCTTCAATATACATATATGAAATTTCCAGCGG	978
Db	901	TCCCTCTTGGCAGAGGGAACTTCTGCGAAGACCTTCAATATACATATATGAAATTTCCAGCGG	960
QY	979	TTTTTGAATTTTCAAGATGACCCCAAGAGAGAGAGACTTCTTCTGATCTGATTTCAAAGC	1033
Db	961	TTTTTGAATTTTCAAGATGACCCCAAGAGAGAGAGACTTCTTCTGATCTGATTTCAAAGC	1020
QY	1039	TTGTTGTGCGGCGCAAGAAAGAGACTGAAGTTTGAAGTCTTTTGTGCTGCATCTTTCTTC	1098
Db	1021	TTGTTGTGCGGCGCAAGAAAGAGACTGAAGTTTGAAGTCTTTTGTGCTGCATCTTTCTTC	1080
QY	1099	TCTAAATTTGACTGGAACAACATTTGTGTAATCTTCTCTCCCTCTTGTTTCCACCTCTCAAG	1155
Db	1081	TCTAAATTTGACTGGAACAACATTTGTGTAATCTTCTCTCCCTCTTGTTTCCACCTCTCAAG	1144
QY	1159	TCTGACGATGACACCTCCAAATTTTATGTAACAGAGAAAGAAATTCGAGGGTTTCACTCTCT	1212
Db	1141	TCTGACGATGACACCTCCAAATTTTATGTAACAGAGAAAGAAATTCGAGGGTTTCACTCTCT	1200
QY	1219	CCGTGCTCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTTGTGCGGGATTTTTCG	1278
Db	1201	CCGTGCTCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTTGTGCGGGATTTTTCG	1260
QY	1279	TACAGCAAGGCACCTGGGGATTTTGTGTGATATGTAGTCTGTTGTGTGCGGGTCTGGACATCC	1333
Db	1261	TACAGCAAGGCACCTGGGGATTTTGTGTGATATGTAGTCTGTTGTGTGCGGGTCTGGACATCC	1320
QY	1339	CTGTGCAAGACTGACTCCATATGGAATAAGAACTTCTCATCAAAAGCAAAGACTACAGAC	1398
Db	1321	CTGTGCAAGACTGACTCCATATGGAATAAGAACTTCTCATCAAAAGCAAAGACTACAGAC	1380
QY	1399	TCTCAGGACAAAGTGTCAACAAGTGAAGAGAAATGAAACCCGGTTTCACTCGAGAGTGTCA	1458
Db	1381	TCTCAGGACAAAGTGTCAACAAGTGAAGAGAAATGAAACCCGGTTTCACTCGAGAGTGTCA	1440
QY	1459	GAGGTGAGGCTGTGCTTATGTCAGAAAGAGGTGAGCTGAAGGCTCTGAGACTCAGAGA	1518
Db	1441	GAGGTGAGGCTGTGCTTATGTCAGAAAGAGGTGAGCTGAAGGCTCTGAGACTCAGAGA	1500
QY	1519	TTCCTCTCTGAGACAGAACTTGTCTATCTTACATCACAGATATCAGTAGCTTAAAGCAAGT	1578
Db	1501	TTCCTCTCTGAGACAGAACTTGTCTATCTTACATCACAGATATCAGTAGCTTAAAGCAAGT	1560

QY	1579	TTGGAGCAAGCAACGATGGAGGTGTCCAGAGGATGACAAAGCATGCGAGCTTCTCCAT	163
Db	1561	TTGGAGCAAGCAACGATGGAGGTGTCTCCAGAGGATGACAAAGCATGCGAGCTTCTCCAT	1620
QY	1639	GATATCAGAGACACAGCCGGAAGCTCCAAAGAAATCAAAGAGCAGAGATACAGGCTCA	1699
Db	1621	GATATCAGAGACACAGCCGGAAGCTCCAAAGAAATCAAAGAGCAGAGATACAGGCTCA	1688
QY	1699	GTGGAAAGAAATGAGGTTGATGATCACTTGGAAAGAGATCTTGTCTCAGCAAGAA	1755
Db	1681	GTGGAAAGAAATGAGGTTGATGATCACTTGGAAAGAGATCTTGTCTCAGCAAGAA	1740
QY	1759	CGAGTGTATCTAGGAATCTAGGCTGAGAGATCTCGGCTTGGCTGAAGAAATTCAG	1818
Db	1741	CGAGTGTATCTTAGGAATCTAGGCTGAGAGATCTCGGCTTGGCTGAAGAAATTCAG	1800
QY	1819	CGGAAGCGACAGAAATGTACATTAACCTGTTAAGGCTTAAGAGATCAAGGAAGGCTGA	1878
Db	1801	CGGAAGCGACAGAAATGTACATTAACCTGTTAAGGCTTAAGAGATCAAGGAAGGCTGA	1866
QY	1879	GTGGAGGAATATAGCGAAATCTGAGAGAGATCAATGCTGAGCAGAGCTCAAAATTCAGAG	1938
Db	1861	GTGGAGGAATATGCGAAATCTGAGAGAGATCAATGCTGAGCAGAGCTCAAAATTCAGAG	1920
QY	1939	CTCCAAAGAAACTGGAGAGGCTGCCAAGAGCGAGCCGAGAGGAGACTGAGAGAGCTG	1998
Db	1921	CTCCAAAGAAACTGGAGAGGCTGCCAAGAGCGAGCCGAGAGGAGACTGAGAGAGCTG	1980
QY	1999	CAGAACCCAGAGAGATCTTCTTGAAAGGATCAAGAAAGAGCTGTGTGAAGCTGAGAGAGC	2058
Db	1981	CAGAACCCAGAGAGATCTTCTTGAAAGGATCAAGAAAGAGCTGTGTGAAGCTGAGAGAGC	2040
QY	2059	CGCCATTTCTCGAGAGAACAGGTAAAGAGACTAGAGACATGAGACGTGAGAGAAACGA	2118
Db	2041	CGCCATTTCTCGAGAGAACAGGTAAAGAGACTAGAGACATGAGACGTGAGAGAAACGA	2100
QY	2119	CTGAAGAGATGACATTCAGACAAAATCCACAGATCCAGAGATGGCTGATTAATTCGTG	2178
Db	2101	CTGAAGAGATGACATTCAGACAAAATCCACAGATCCAGAGATGGCTGATTAATTCGTG	2160
QY	2179	GAGCTCGAAGGAAACATCGGAGAGCCCAATCTCAGGCCAGACCTAGAGAGTCAACTG	2238
Db	2161	GAGCTCGAAGGAAACATCGGAGAGCCCAATCTCAGGCCAGACCTAGAGAGTCAACTG	2220
QY	2239	AAACAGAAAGAGCAGACTATGAGAAAAGTTAAAGTGTGGACAATTCAGATTAAGAA	2298
Db	2221	AAACAGAAAGAGCAGACTATGAGAAAAGTTAAAGTGTGGACAATTCAGATTAAGAA	2280
QY	2299	GACCTGCGTGCAGAGGAGACATTCGAGAACATGATTCAGAGACACAGAGAGAGGCCAT	2358
Db	2281	GACCTGCGTGCAGAGGAGACATTCGAGAACATGATTCAGAGACACAGAGAGAGGCCAT	2340
QY	2359	GAGAAAGGCAAAATTTCTCAGCGAACAGAAAGCGATGATCAATGCTATAGGATTCAGAGTC	2418
Db	2341	GAGAAAGGCAAAATTTCTCAGCGAACAGAAAGCGATGATCAATGCTATAGGATTCAGAGTC	2400
QY	2419	AGATTCCTCGAAGCAGAGATTTGTGAACTGTCTGAGCCATTAACCTTGACAGCAATATGC	2478
Db	2401	AGATTCCTCGAAGCAGAGATTTGTGAACTGTCTGAGCCATTAACCTTGACAGCAATATGC	2460
QY	2479	AGTCTTTTAAACCAAAGAACATGAAAGGCCCAAGAAAGATGATTTCTGAATCTCAGGCAA	2538
Db	2461	AGTCTTTTAAACCAAAGAACATGAAAGGCCCAAGAAAGATGATTTCTGAATCTCAGGCAA	2520
QY	2539	CAGAAATTTTAACTTGAGACACAGGCTGGAGAGTTGAGGCCAGAAACGAAACCTGAG	2598
Db	2521	CAGAAATTTTAACTTGAGACACAGGCTGGAGAGTTGAGGCCAGAAACGAAACCTGAG	2580
QY	2599	GAGGAGCTGAGAAAGATCAAGCCACCAAGACACAGATGACAAAGATGGGCTGTGGAACCTG	2658
Db	2581	GAGGAGCTGAGAAAGATCAAGCCACCAAGACACAGATGACAAAGATGGGCTGTGGAACCTG	2640
QY	2659	GAGCAAGATTGGCGGAGGTCACTCTTAGAGCAGAGAGCAGAGAACTGAGAGCTCAAGCGC	2718

Db 2641 GAGACAAGATTGGGGAGGTCACTTAGAGCAGAGAGCAGAAACTGGAGCTCAAGCCG 2700
Qy 2719 CAGCTCAAGAGCTTAACGCTCTCTGCAAGAGCGGAGTCAACATTGACAGCCCTGCAAG 2778
Db 2701 CAGCTCAAGAGCTTAACGCTCTCTGCAAGAGCGGAGTCAACATTGACAGCCCTGCAAG 2760
Qy 2779 GCTGCAAGGCGGCGCTGGAGAGCAGCTTGGCAGGCGAAGCAGAGCTGGAGAGAGCC 2838
Db 2761 GCTGCAAGGCGGCGCTGGAGAGCAGCTTGGCAGGCGAAGCAGAGCTGGAGAGAGCC 2820
Qy 2839 ACAGCAGAAAGCTGAGAGAGAGATCCAGGCACTACCGGCACTAGAGTGAATCCAGCGC 2898
Db 2821 ACAGCAGAAAGCTGAGAGAGAGATCCAGGCACTACCGGCACTAGAGTGAATCCAGCGC 2880
Qy 2899 AATATTGATGCTCTTGTGTAACAGCTGTACTGTATATCAAGAGCTGGAGAGAGCTTAAC 2958
Db 2881 AATATTGATGCTCTTGTGTAACAGCTGTACTGTATATCAAGAGCTGGAGAGAGCTTAAC 2940
Qy 2959 CAGCTGACGAGAGCAGACGCTGAACCTCAACAACTTTCTTATCTTGTCCAAACAATC 3018
Db 2941 CAGCTGACGAGAGCAGACGCTGAACCTCAACAACTTTCTTATCTTGTCCAAACAATC 3000
Qy 3019 GATGAGGCTTCTGGCCGCAACGAGAGATTGTAACAATGCGAAGTGAAGTGAACATCTC 3078
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Qy 3079 CGCGGAGAGATCAAGAGCAGAGATGACGCTTACAGCCAGAGCAAAAGATGAGGCT 3138
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Db 3181 GAGCTGCTAGAAAAAAGCGGCGAGTGGAGGCTTGGAGAGAGCTCTGGGATGATGAGAA 3240
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Db 3361 GAGCAAAAGGCTGAGATTCTGCTCTGACAGAGGCTCTCAAGAGCAGAGAGCTGAGAGCC 3420
Qy 3439 GAGAGCTTCTGACAAAGCTCAATGACCTGAGAGAAAGCATGCTTATGCTTGAATGAAT 3498
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Db 3601 CAAAGCTGCAAGAGCTTGAATCGGGCTGATCTA CTGAGACAGAGAAAGAGTGAATTG 3660
Qy 3679 GAGTATCACTGGAAGAAATTCAGGTTCTCTATTCATGAAAGGTGAAGTGAAGGC 3738
Db 3661 GAGTATCACTGGAAGAAATTCAGGTTCTCTATTCATGAAAGGTGAAGTGAAGGC 3720
Qy 3739 ACTATTTCTCAACAACTCAATGATTTTCTGCAAGCCAAATGAGCAACTGCT 3798

Db 3721 ACTATTTCTCAACAACTCAATGATTTTCTGCAAGCCAAATGAGCAACTGCT 3780
Qy 3799 AAAAAAAGAGGTTTATTAGTGAAGGAAAGAGACCTTGTATCCCAACAGGTT 3858
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Db 3841 CCTCTGATGACAAATGAGCTGAGAGCTGAGGCTTGGAGAAAGAGAGCTGCTGTGAGAG 3900
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Qy 4219 AAGTGTGCTGT 4278
Db 4201 AAGTGTGCTGT 4260
Qy 4279 TGTCAAGTATGT 4338
Db 4261 TGTCAAGTATGT 4320
Qy 4339 GCTGAATATGCAACACTTCAACCGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4398
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Db 4621 AATTAAGCCAAAGCAGAAAGCAGAGCTGATGCTAAATCTGCTGGAATCTCCCTGCTG 4680
Qy 4699 AAATGGAAGGTGATGACCGTCTAAGCATGAATGCAAGCTGCTCCCTCAAGTGAAGTG 4758
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Qy 4759 GT 4818
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5281 CCTGTCTCAATGTGAGGTGAACAGCGAGGGCAGCGAGAGTACTGTGTGTTC 5340
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5341 CAGCAATTTGAGGTGTCTGTGATTTCTTACGAAAGCTAGAGCCGACAGACATCTCAAG 5400
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5881 ATGCTCAGCAGCGGAGAGAGCGGTCCCGCGGAGAGGCTTTGAAGACAGAGAGCGGCG 5940

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DB 5941 CGGCTGCTGCGGAGAGCCGTGAGACCCCGCTGTCTCCAGGTGACCAAGGAAAGAGCGCAG 6000
QY 6019 AGTGCTCTCAAGTTTCAAGGTTAAACGTGCACTTATTAATGACTGGAATTAAGACTG 6078
DB 6001 AGTGCTCTCAAGTTTCAAGGTTAAACGTGCACTTATTAATGACTGGAATTAAGACTG 6060
QY 6079 GACAACTGCGCAGCTAATGCTGCTGAGATCATTCAGCTGATGAGAGAAATCCGG 6138
DB 6061 GACAACTGCGCAGCTAATGCTGCTGAGATCATTCAGCTGATGAGAGAAATCCGG 6120
QY 6139 CAGCAGGTTGAAGAGTGTCTGTGAGACAGATTAATGCTGA 6180
DB 6121 CAGCAGGTTGAAGAGTGTCTGTGAGACAGATTAATGCTGA 6162

RESULT 5

US-10-017-216-3
Sequence 3, Application US/10017216
Publication No. US20020160483A1
GENERAL INFORMATION:
APPLICANT: KAPILLER-LIBERMAN, Rosana
TITLE OF INVENTION: 13245, A No. US20020160483A1e1 Human Myotonic Dysretrophy Type Prot
TITLE OF INVENTION: Kinase and Uses Therefor
FILE REFERENCE: 10147-5701
CURRENT APPLICATION NUMBER: US/10/017, 216
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 60/242, 429
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 6159
TYPE: DNA
ORGANISM: Homo sapiens
US-10-017-216-3

Query Match 93.74; Score 6159; DB 13; Length 6159;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 6159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ATGTTGAAGTTCAAAATATGAGAGCGGAAATCTTTGATGCTGAGTGTGAAACCCATT 78
DB 1 ATGTTGAAGTTCAAAATATGAGAGCGGAAATCTTTGATGCTGAGTGTGAAACCCATT 60
QY 79 GCCAGCGGCGCTTCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGACTCA 138
DB 61 GCCAGCGGCGCTTCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGACTCA 120
QY 139 CAGCAGATGTCCTCTTTTCCGAGAGGATATTAATGAGCCCTTTGTTCTTTGAA 198
DB 121 CAGCAGATGTCCTCTTTTCCGAGAGGATATTAATGAGCCCTTTGTTCTTTGAA 180
QY 199 GAATGAGTCAAGCTGCTGATGAAGATTAAGCAGTGAACAATTGTCGGAAGTAT 258
DB 181 GAATGAGTCAAGCTGCTGATGAAGATTAAGCAGTGAACAATTGTCGGAAGTAT 240
QY 259 TCCGACACCATGATGATTAAGAGCTCCAGCTTTCGCAAGAGACTTGAAGTCA 318
DB 241 TCCGACACCATGATGATTAAGAGCTCCAGCTTTCGCAAGAGACTTGAAGTCA 300
QY 319 AGCTTGAAGTGTGATCTTGTGCAAGTGAAGTGTGAAGAGAGAGAGAGAGAGAGAGAG 378
DB 301 AGCTTGAAGTGTGATCTTGTGCAAGTGAAGTGTGAAGAGAGAGAGAGAGAGAGAGAG 360
QY 379 GACATCTATGATGAAGTGAAGAGAGAGCTTTATTTGCGCAGAGCAGGTTTCA 438
DB 361 GACATCTATGATGAAGTGAAGAGAGAGCTTTATTTGCGCAGAGCAGGTTTCA 420
QY 439 TTTTGAAGAGAGCGGAAACATTTATCTGAGACCAAGCCGCTGATCCCAATTA 498
DB 421 TTTTGAAGAGAGCGGAAACATTTATCTGAGACCAAGCCGCTGATCCCAATTA 480

OY	439	CAGTATGCGCTTTCAGAGCAAAAAATCACTTTATCTGATGAGAGAAATATCACTGCTGAGGG	558
Db	481	CAGTATGCGCTTTCAGAGCAAAAAATCACTTTATCTGATGAGAGAAATATCACTGCTGAGGG	540
OY	559	GACTTGCTGTCACTTTGATATGATATATGAGCAACGATTAGATGATAAACTGTATCACTTT	618
Db	541	GACTTGCTGTCACTTTGATATGATATATGAGCAACGATTAGATGATAAACTGTATCACTTT	600
OY	619	TAqCTTAGCTGAGCTGATTTTGGCTGTTCACAGCTTCAITCTGATGGATACGTGATCGA	678
Db	601	TAGCTTAGCTGAGCTGATTTTGGCTGTTCACAGCTTCAITCTGATGGATACGTGATCGA	660
OY	679	GAGATCAAGCCGAGAGACATCTCGTGAACCGCACAGACACATCAACCTGCTGGAATTTT	738
Db	661	GACATCAAGCCGAGAGACATCTCGTGAACCGCACAGACACATCAACCTGCTGGAATTTT	720
OY	739	GGATCTGCGCGCAAAATGATTTCAAAACAAGATGTGAAATGCGCAACTCCGATTTGGAGC	798
Db	721	GGATCTGCGCGCAAAATGATTTCAAAACAAGATGTGAAATGCGCAACTCCGATTTGGAGC	780
OY	799	CCAAGTTATCATGCGCTCTGGAATGTGACTGTGATGAAACGGGATATGAAAAAGCACCTAC	858
Db	781	CCAAGTTATCATGCGCTCTGGAATGTGACTGTGATGAAACGGGATATGAAAAAGCACCTAC	840
OY	859	GGCCTGGAAGCTGTGACTGGGCGTCACTGAGCGCGTGAATGCTATAGATGATATTTATGGAGA	918
Db	841	GGCCTGGAAGCTGTGACTGGGCGTCACTGAGCGCGTGAATGCTATAGATGATATTTATGGAGA	900
OY	919	TCqCCCTTTCGAGAGGGAACTCTGCGCAAGACCTTCAATPAACATTATGAATTTCCAGCGG	978
Db	901	TCqCCCTTTCGAGAGGGAACTCTGCGCAAGACCTTCAATPAACATTATGAATTTCCAGCGG	960
OY	979	TTTTTGAAATTTCCAGATGACCCCAAGAGACAGTGACTTTCTTGATCTGATTCAAAGC	1038
Db	961	TTTTTGAAATTTCCAGATGACCCCAAGAGTGAAGTGAATTTCTTGATCTGATTCAAAGC	1020
OY	1039	TTGTTGTGCGGCAGAGAAAGAGACTGAAGTTTGAAGTCTTTGCTGCATCTTTCTTC	1098
Db	1021	TTGTTGTGCGGCAGAGAAAGAGACTGAAGTTTGAAGTCTTTGCTGCATCTTTCTTC	1080
OY	1099	TCCTAAATTTGACTGGAACAACATTCTGTAACTCTCTCTCCCGCTTGTTCCACCTCTCAG	1158
Db	1081	TCCTAAATTTGACTGGAACAACATTCTGTAACTCTCTCTCCCGCTTGTTCCACCTCTCAG	1140
OY	1159	TCTGACGATGACACCTCCCAATTTTATGAAACAAGAGAAATGCTGGGGTTTAACTCCCT	1218
Db	1141	TCTGACGATGACACCTCCCAATTTTATGAAACAAGAGAAATGCTGGGGTTTAACTCCCT	1200
OY	1219	CCGTGCGAGCTGAGCGCCCTCAAGCTTCTCGGGTGAAGAACTGCGCTTTGTGGGGTTTTCG	1278
Db	1201	CCGTGCGAGCTGAGCGCCCTCAAGCTTCTCGGGTGAAGAACTGCGCTTTGTGGGGTTTTCG	1260
OY	1279	TACAGCAAGGCACTGGGGATCTTGTTGTATCTGATGCTGTGTGCTGGGCTGGAACCTC	1338
Db	1261	TACAGCAAGGCACTGGGGATCTTGTTGTATCTGATGCTGTGTGCTGGGCTGGAACCTC	1320
OY	1339	CCTGCGCAAGACTAGCTCCATGGAAAAAGAACTTCTCATCAAAAGCAAGAGCTACAGAC	1398
Db	1321	CCTGCGCAAGACTAGCTCCATGGAAAAAGAACTTCTCATCAAAAGCAAGAGCTACAGAC	1380
OY	1399	TCTCAGAGCAAGTGTCAACAATGGAAGCAAGAAATGACCCCGTTTCAATCGAGAGTGTCA	1458
Db	1381	TCTCAGAGCAAGTGTCAACAATGGAAGCAAGAAATGACCCCGTTTCAATCGAGAGTGTCA	1440
OY	1459	GAGGTGAGAGCTGTCTTATGTCAGAGAGAGGTGAGCTGAAGGCTCTGAGACTCAGAGA	1518
Db	1441	GAGGTGAGAGCTGTCTTATGTCAGAGAGAGGTGAGACTGAAGGCTCTGAGACTCAGAGA	1500
OY	1519	TCqCTCTCTGAGAGAGACCTTGTCTACTTACATCAACAATGACAGTACTTAAAGCAAGT	1578
Db	1501	TCqCTCTCTGAGAGAGACCTTGTCTACTTACATCAACAATGACAGTACTTAAAGCAAGT	1560

QY	1579	TTGAGCAGACGACCGGATGAGGTGTCCTCCAGGAGATGACAAAGACCTGCACTTCTCCAT	1638
Db	1561	TTGGAGCAGACCGGATGAGGTGTCCTCCAGGAGATGACAAAGACCTGCACTTCTCCAT	1620
QY	1639	GATATCAGAGAGCAGAGCCGGAGGCTCCAAAGAAATCAAAGAGCAGAGATACCAAGCTCAA	1698
Db	1621	GATATCAGAGAGCAGAGCCGGAGGCTCCAAAGAAATCAAAGAGCAGAGATACCAAGCTCAA	1688
QY	1699	GTGGAGAAATGAGGTTGATGATGAAATCAGTTGGAGAGATCTTTGTCTCAGCAGAGAGA	1758
Db	1681	GTGGAGAAATGAGGTTGATGATGAAATCAGTTGGAGAGATCTTTGTCTCAGCAGAGAGA	1740
QY	1759	CGGAGTGATCTCTAGCAATCTGAGCTGAGAGATCTCGGCTTGCTGCTGAAGAAATTCAG	1818
Db	1741	CGGAGTGATCTCTAGCAATCTGAGCTGAGAGATCTCGGCTTGCTGCTGAAGAAATTCAG	1800
QY	1819	CGGAAAGGAGCAGAGATGTCAGCATTAATCTGTGAAGCTTAAGGATCAAAGGAGGCTGAA	1878
Db	1801	CGGAAAGGAGCAGAGATGTCAGCATTAATCTGTGAAGGCTTAAGGATCAAAGGAGGCTGAA	1866
QY	1879	GTGGAGAAATATGCGAAACTGAGAGAGATCAATGCTGAGCAGCAGCTTCAAAATTCAGGAG	1938
Db	1861	GTGGAGAAATATGCGAAACTGAGAGAGATCAATGCTGAGCAGCAGCTTCAAAATTCAGGAG	1920
QY	1939	CTCCAGAGAAATCTGAGAGAGGCTGCAAAAGAGCGAGCCGAGAGGAGCTGAGAGAGCTG	1998
Db	1921	CTCCAGAGAAATCTGAGAGAGGCTGCAAAAGAGCGAGCCGAGAGGAGCTGAGAGAGCTG	1980
QY	1999	CAGAAACGAGAGGATTTCTTCTGAAGGCACTCAAGAAAGAAAGCTGTGTGAAGCTGAGAGAGC	2058
Db	1981	CAGAAACGAGAGGATTTCTTCTGAAGGCACTCAAGAAAGAAAGCTGTGTGAAGCTGAGAGAGC	2040
QY	2059	CGCCATTCTCTGAGAGACAGAGTAAAGAGACTAGAGACCATGAGCGCTAGAGAAAACAGA	2118
Db	2041	CGCCATTCTCTGAGAGACAGAGTAAAGAGACTAGAGACCATGAGCGCTAGAGAAAACAGA	2100
QY	2119	CTGAAGATGACATCCAGACAAAAATCCCAAGATCCAGCAGATGCGCTGATPAAATTTCTG	2178
Db	2101	CTGAAGATGACATCCAGACAAAAATCCCAAGATCCAGCAGATGCGCTGATPAAATTTCTG	2160
QY	2179	GAGCTCGAGAGGAAACATCGGAGAGGCCCAATCTCAGCCGAGCACTTAGAGTGCACCTG	2238
Db	2161	GAGCTCGAGAGGAAACATCGGAGAGGCCCAATCTCAGCCGAGCACTTAGAGTGCACCTG	2220
QY	2239	AAACAGAAAGAGCAGACCTATGAGAGAAAAGATTAAAGTTGGACAATCAGATPAAAGAA	2298
Db	2221	AAACAGAAAGAGCAGACCTATGAGAGAAAAGATTAAAGTTGGACAATCAGATPAAAGAA	2280
QY	2299	GACCTGCTGACAGAGAGACACTGAGAGACATGATGACAGAGACACAGAGAGAGGCCAT	2358
Db	2281	GACCTGCTGACAGAGAGACACTGAGAGACATGATGACAGAGACACAGAGAGAGGCCAT	2340
QY	2359	GAGAAAGGCAAAATTTCTCAGCGAACAGAGGCCGATGATCAATGCTATGAGATTTCCAAATTC	2418
Db	2341	GAGAAAGGCAAAATTTCTCAGCGAACAGAGGCCGATGATCAATGCTATGAGATTTCCAAATTC	2400
QY	2419	AGATCCCTCGAAGCAGAGGATGTGTGAACTGTCTGAAAGCCAAATTAATCTGACGAAATAGC	2478
Db	2401	AGATCCCTCGAAGCAGAGGATGTGTGAACTGTCTGAAAGCCAAATTAATCTGACGAAATAGC	2460
QY	2479	AGTCTTTTATCCCAAAGGACATGAGAGGCCCAAGAGAGATGATTTCTGAATCTCAGGCAA	2538
Db	2461	AGTCTTTTATCCCAAAGGACATGAGAGGCCCAAGAGAGATGATTTCTGAATCTCAGGCAA	2520
QY	2539	CAGAAATTTTATCTCTGAGACACAGGCTGTGGAAAGTTGAGAGGCCCAAGAACTGGAG	2598
Db	2521	CAGAAATTTTATCTCTGAGACACAGGCTGTGGAAAGTTGAGAGGCCCAAGAACTGGAG	2580
QY	2599	GAGCAGCTGAGAGAGATCAGCCACCAAGACCAAGCAGTGCAAAGAAATCGGCTGTGAAATCTG	2658
Db	2581	GAGCAGCTGAGAGAGATCAGCCACCAAGACCAAGCAGTGCAAAGAAATCGGCTGTGAAATCTG	2640
QY	2659	GAGCAGAAATTCGAGAGGTCAGTCTGAGACCGAGAGACAGAAATCGAGCTCAAGGCT	2718

Db 2641 GAGACAAAGATTGGGGAGGTCAAGTCTAAGCAAGAGAGAGAAACTGGAGCTCAAGCCG 2700
QY 2719 CAGCTCACAGAGCTAAGCTCTCCCTGCAAGAGCGGAGTCAAGTTTGAAGCCCTGCGAG 2778
Db 2701 CAGCTCACAGAGCTAAGCTCTCCCTGCAAGAGCGGAGTCAAGTTTGAAGCCCTGCGAG 2760
QY 2779 GCTGCACGGGCGGCTCTGGAAGAGCAGCTTCGCGCAGCGGAGAAGAGCTGGAAAGAGCC 2838
Db 2761 GCTGCACGGGCGGCTCTGGAAGAGCAGCTTCGCGCAGCGGAGAAGAGCTGGAAAGAGCC 2820
QY 2839 ACGAGAAAGCTTGAAGAGAGATCCAGCACTTCACGGCACTATGAGATGAATCCAGCGC 2898
Db 2821 ACGAGAAAGCTTGAAGAGAGATCCAGCACTTCACGGCACTATGAGATGAATCCAGCGC 2880
QY 2899 AAATTGATGCTCTCTGTAACAGCTGTACTGTAACTACAGACCTTGAAGAGAGAGCTTAAC 2958
Db 2881 AAATTGATGCTCTCTGTAACAGCTGTACTGTAACTACAGACCTTGAAGAGAGCTTAAC 2940
QY 2959 CAGCTGACCGAGAGCAACCGCTGAATCAACAACCAAACTTCTACTTGTCCAAAACAATC 3018
Db 2941 CAGCTGACCGAGAGCAACCGCTGAATCAACAACAACCAAACTTCTACTTGTCCAAAACAATC 3000
QY 3019 GATGAGGCTTTGCGCGCCAAACGAGATTTGTAACAATGCGAAGTGAAGTGAACATCTC 3078
Db 3001 GATGAGGCTTTGCGCGCCAAACGAGATTTGTAACAATGCGAAGTGAAGTGAACATCTC 3060
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Db 3061 CCGCGGGAATATCACGGAAGAGAGATGCAAGCTTACAGGCAAGAAAGCAATGAGGCT 3120
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Db 3121 CTGAAGACCAAGTGCACATGCTGAGAGAAAGAGTATGATTTGAGGCGCTTAACGAT 3180
QY 3199 GAGCTGCTAGAAAAAGAGCGGCAATGAGAGCCCTGAGAGAGCGTCTGAGTATGAGAAA 3258
Db 3181 GAGCTGCTAGAAAAAGAGCGGCAATGAGAGCCCTGAGAGAGCGTCTGAGTATGAGAAA 3240
QY 3259 TCCCAATTGAGATGTCGGGTTGAGAGCTGCAAGAAATGCTGGAACCCAGAAACAGAGC 3318
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QY 3379 GAGCAACAAGCTGAGATTTCTCGCTGCGCAGAGCTCTCAAAAGACAGAACTGAAAGCC 3438
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QY 3439 GAGAGCTCTGCAACAAGCTCAATGACCTGGAAGAAAGCATGCTATGCTTGAATGAAT 3498
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QY 3499 GCCCGAAGCTTACAGCAAGAGCTGAGACTGAACGAGAGCTCAACAGAGGCTTCTGAA 3558
Db 3481 GCCCGAAGCTTACAGCAAGAGCTGAGACTGAACGAGAGCTCAACAGAGGCTTCTGAA 3540
QY 3559 GAGCAAGCCAAATTACAGCAAGAGATGACCTGCAAGAAATACATTTTCCGCTGACT 3618
Db 3541 GAGCAAGCCAAATTACAGCAAGAGATGACCTGCAAGAAATACATTTTCCGCTGACT 3600
QY 3619 CAAGGCTGCAAGAGCTTAAGATCGGGCTGATCTACAGAGCAAGAAAGATGACTTG 3678
Db 3601 CAAGGCTGCAAGAGCTTAAGATCGGGCTGATCTACAGAGCAAGAAAGATGACTTG 3660
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Db 3721 ACTATTTCTCAACAAACCAACTCATTTGATTTTCTGCAAGCCAAATGAGCAACCTGCT 3780
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Db 4381 CTCAGAACCAAGAGCCCGACAGCAGCTTGCACCTGGAAGGCTGATGAAGTGCACAG 4440
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QY 4639 AATTAACCAAGCAAGAAAAAGCAGAACTGATGTTAACTGCTTGAAGCTCCCTGCTG 4698
Db 4621 AATTAACCAAGCAAGAAAAAGCAGAACTGATGTTAACTGCTTGAAGCTCCCTGCTG 4680
QY 4699 AAACCTGAAGAGATGACAGTCTGACATGAACCTGCAAGCTGCGCTTCAGTGAACAGGAG 4758
Db 4681 AAACCTGAAGAGATGACAGTCTGACATGAACCTGCAAGCTGCGCTTCAGTGAACAGGAG 4740
QY 4759 GTGTGTGAGGACCGAGAGAGGCTCTACGCGCTGAAATGCTTTGAAAACTCCCTAAAC 4818
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QY 4819 CATGTCCAGGAATTTGAGAGCTTCCAAATTTATATTAATCAAGAGCTGAGAGAGCTA 4878
Db 4801 CATGTCCAGGAATTTGAGAGCTTCCAAATTTATATTAATCAAGAGCTGAGAGAGCTA 4860


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: LENGTH: 6298
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incycle ID No. US20040053394A1 7484498CB1
US-10-011-43

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Query Match      86.5%; Score 5684.4; DB 17; Length 6298;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 5979; Conservative 0; Mismatches 36; Indels 243; Gaps 3;

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QY 61 GGTGCTGCTGAACCCATTCGCAAGCCGCGCTTCAGAGCTGATCTTTCTTCAGAGGAAA 120
Db 97 GGTGCTGCTGAACCCATTCGCAAGCCGCGCTTCAGAGCTGATCTTTCTTCAGAGGAAA 156
QY 121 CCAACCTTTATGACTCAAGACAGATGTCCTCTTCCCGAAGAGGATTTAGATGCC 180
Db 157 CCAACCTTTATGACTCAAGACAGATGTCCTCTTCCCGAAGAGGATTTAGATGCC 216
QY 181 CTCTTTGTTCTCTTTGAAGATGCAAGCTGCTCTGATGAAGATTAAAGCACTGAGC 240
Db 217 CTCTTTGTTCTCTTTGAAGATGCAAGCTGCTCTGATGAAGATTAAAGCACTGAGC 276
QY 241 AACTTTGTCCGGAAGTATTCGCAACCATATGCTGAAGTTACAGAGCTCCAGCTTCGCGA 300
Db 277 AACTTTGTCCGGAAGTATTCGCAACCATATGCTGAAGTTACAGAGCTCCAGCTTCGCGA 336
QY 301 AAGACCTTCGAAGTCAAGAGTCTTTGAGGTTGATGCTTTCGTAAGTGAAGGCTTATATG 360
Db 337 AAGACCTTCGAAGTCAAGAGTCTTTGAGGTTGATGCTTTCGTAAGTGAAGGCTTATATG 396
QY 361 AAGAGAAAAGCAACCGGGAATCTATGCTATGAAGATGATGAAGAAAGGCTTATATG 420
Db 397 AAGAGAAAAGCAACCGGGAATCTATGCTATGAAGATGATGAAGAAAGGCTTATATG 456
QY 421 GCCAGAGACAGGTTTCATTTTTGAAGAGCGGAATATATATCTGTAAGCACAGC 480
Db 457 GCCAGAGACAGGTTTCATTTTTGAAGAGCGGAATATATATCTGTAAGCACAGC 516
QY 481 CCGTGATCCCCCAATTACAGTATGCTTTCAAGCAAAAATCACTTTATCTGATGAG 540
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QY 601 GAAAACTGATACAGTTTAACTAGCTGAGTATTTGGCTGTCAAGGCTTATATG 660
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QY 661 ATGGATATGCTGATCGAGACATCAAGCTGAGCAATTCGTTGACCGACAGAGAC 720
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QY 841 GATGGAAGAGCACTTAAGGCTTGAAGTGTGAAGTGTGAAGGCTGAT 900
Db 877 GATGGAAGAGCACTTAAGGCTTGAAGTGTGAAGTGTGAAGGCTGAT 936
QY 901 GAGATGATTTATGGAGATCCCTTCGACAGAGGAACTCTGCAAGAACTTCAATAC 960

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Db 1777 CTTGCTCAGCAAGAAAGAGGAGTCTTACGAATCTGAGCTGAGAGCTTCCGCTT 1836
QY 1801 GCTGCTGAAGATTCAGCGGAAAGCAGAAATGTCAGCATTAACCTGTTGAAGCTAAG 1860
Db 1837 GCTGCTGAAGATTCAGCGGAAAGCAGAAATGTCAGCATTAACCTGTTGAAGCTAAG 1896
QY 1861 GATCAAGGAGAGCTTGAAGTGAAGAAATGTCAGAACTGAGAAATCAATGCTGAGCAG 1920
Db 1897 GATCAAGGAGAGCTTGAAGTGAAGAAATGTCAGAACTGAGAAATCAATGCTGAGCAG 1956
QY 1921 CAGCTCAAAATTCAGAGCTCCAGAGAACTGAGAAAGCTT----- 1962
Db 1957 CAGCTCAAAATTCAGAGCTCCAGAGAACTGAGAAAGCTTAAACCTGAGCAGCAG 2016
QY 1963 -----GCAAGAGAGCAGCCGAGAGGAGCTGAG 1992

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Db 2017 GCCACGAGCTGCTGCAATATCCGCCAGGCAAGGAGCGACCGAGAGGAGCTGGAG 2076
Qy 1993 AAGCTCAGAAACGAGAGGATTTCTCTGAAGGATCATGAAAGAAAGCTGCTGGAAGCTGGAG 2052
Db 2077 AAGCTCAGAAACGAGAGGATTTCTCTGAAGGATCATGAAAGAAAGCTGCTGGAAGCTGGAG 2136
Qy 2053 GAAAGCGGCAATCTCTGAGAGAACAAAGTAAAGAGCTAGAGACCATGAGCCTTAGAGAA 2112
Db 2137 GAAAGCGGCAATCTCTGAGAGAACAAAGTAAAGAGCTAGAGACCATGAGCCTTAGAGAA 2196
Qy 2113 AACAGACTGAAGATGATCATCCAGACAAATTCCTCAACAGATCCAGCAGATGCTGATTA 2172
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Qy 2173 ATTCTGAGCTGCAAGAGAAACATTCGGGAGGCCCAAGTCTCAGCCCAAGCTTAGAAAGT 2232
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Qy 2233 CACCTGAAAACAGAAAGAGCAGCACTATGAGAGAAAGATTAAAGTGTGGAATTCAGAT 2292
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Qy 2713 AAGCGCAGCTCAAGAGCTACAGCTCTCTGCAAGAGCGAGTCAAGTTGACAGCC 2772
Db 2797 AAGCGCAGCTCAAGAGCTACAGCTCTCTGCAAGAGCGAGTCAAGTTGACAGCC 2856
Qy 2773 CTGCAAGCTGCAAGGCGGCGCTGAGAGGCGAGCTTCGCGAGGCGAAGACAGAGCTGGAA 2832
Db 2857 CTGCAAGCTGCAAGGCGGCGCTGAGAGGCGAGCTTCGCGAGGCGAAGACAGAGCTGGAA 2916
Qy 2833 GAGACCAAGCAGAAAGCTGAAGAGAGATCCAGGCACTCAAGCATAGAGATGAATC 2892
Db 2917 GAGACCAAGCAGAAAGCTGAAGAGAGATCCAGGCACTCAAGCATAGAGATGAATC 2976
Qy 2893 CAGCGCAATTTGATGCTCTTGTGTAACAGTGTACTGTATCAAGACCTGAGAGGACG 2952
Db 2977 CAGCGCAATTTGATGCTCTTGTGTAACAGTGTACTGTATCAAGACCTGAGAGGACG 3036
Qy 2953 CTAAACACAGCTGACGAGGACCAAGCTGAACCAACCAAACTTACTTGTGCAAA 3012
Db 3037 CTAAACACAGCTGACGAGGACCAAGCTGAACCAACCAAACTTACTTGTGCAAA 3096
Qy 3013 CAAGCTGATGAGGCTTCTGGCGGCAACGAGATTTGTAACACTGGAAGTGAAGTGAAC 3072
Db 3097 CAAGCTGATGAGGCTTCTGGCGGCAACGAGATTTGTAACACTGGAAGTGAAGTGAAC 3156

Qy 3073 CATCTCCGCGGGAGATCAAGGAAAGAGATGACAGCTTACAGGCGAAGAGCAAAACGATG 3132
Db 3157 CATCTCCGCGGGAGATCAAGGAAAGAGATGACAGCTTACAGGCGAAGAGCAAAACGATG 3216
Qy 3133 GAGGCTCTGAAAGACCAAGTGAACCAATGCTGAGAGAAACAGTCAATGATTTGAGAGCCCTTA 3192
Db 3217 GAGGCTCTGAAAGACCAAGTGAACCAATGCTGAGAGAAACAGTCAATGATTTGAGAGCCCTTA 3276
Qy 3193 AACGATGAGCTCTGAAAGAAAGAGCGAGTGGAGGCTTGGAGAGGCTCTGGGTGAT 3252
Db 3277 AACGATGAGCTCTGAAAGAAAGAGCGAGTGGAGGCTTGGAGAGGCTCTGGGTGAT 3336
Qy 3253 GAGAAATCCCAATTTGAGTGTGGGTGAGAGCTGAGAGAAATGCTGGAACCCAGAAA 3312
Db 3337 GAGAAATCCCAATTTGAGTGTGGGTGAGAGCTGAGAGAAATGCTGGAACCCAGAAA 3396
Qy 3313 CAGAGCAGGCGAGAGCCGATCAGCGGATCAACCGAGTCTGCGCAGGTGGAGCTGGA 3372
Db 3397 CAGAGCAGGCGAGAGCCGATCAGCGGATCAACCGAGTCTGCGCAGGTGGAGCTGGA 3456
Qy 3373 GTGAAGAGCACAGGCTGAGATTTCTGCTCTGAGCAGGCTTCTCAAGAGCAAGACTG 3432
Db 3457 GTGAAGAGCACAGGCTGAGATTTCTGCTCTGAGCAGGCTTCTCAAGAGCAAGACTG 3516
Qy 3433 AAGCGCGAGAGCTCTGAGCAAGCTCAATGACCTGAGAGAAAGATGCTATGCTTGA 3492
Db 3517 AAGCGCGAGAGCTCTGAGCAAGCTCAATGACCTGAGAGAAAGATGCTATGCTTGA 3576
Qy 3493 ATGAATGCCCGAAGCTTACAGAGAGCTGAGAGCTGAGAGCTCAACAGAGGCTT 3552
Db 3577 ATGAATGCCCGAAGCTTACAGAGAGCTGAGAGAGCTGAGAGCTCAACAGAGGCTT 3636
Qy 3553 CTGGAAGAGCAAGCAATTTACAGACAGATGAGACCTGACAGAAATCAATTTCCGT 3612
Db 3637 CTGGAAGAGCAAGCAATTTACAGACAGATGAGACCTGACAGAAATCAATTTCCGT 3696
Qy 3613 CTGACTCAAGGCTGCAAGAACTCTAGATCGGGGTGATCTGCAAGACAAAGAAAGT 3672
Db 3697 CTGACTCAAGGCTGCAAGAACTCTAGATCGGGGTGATCTGCAAGACAAAGAAAGT 3756
Qy 3673 GACTTGAGATCAGCTGGAAGAAACATTCAGGTTCTATTTCTCATGAAAGGTGAAATG 3732
Db 3757 GACTTGAGATCAGCTGGAAGAAACATTCAGGTTCTATTTCTCATGAAAGGTGAAATG 3816
Qy 3733 GAAAGCACTATTTCTCAACAAACCAAACTCATTTGTTCTGCAAGCCAAATGAGCAAA 3792
Db 3817 GAAAGCACTATTTCTCAACAAACCAAACTCATTTGTTCTGCAAGCCAAATGAGCAAA 3876
Qy 3793 CTGCTAAAGAAAGAAAGGTTTATTAGTGAAGGAAAGAGACCTTACCCACA 3852
Db 3877 CTGCTAAAGAAAGAAAGGTTTATTAGTGAAGGAAAGAGACCTTACCCACA 3892
Qy 3853 CAGGTTCTCTGACAGTAAATGAGCTGAGCTGGCCCTGAGAGAGAGAAAGCTGCTGT 3912
Db 3893 -AGGTTCTCTGACAGTAAATGAGCTGAGCTGGCCCTGAGAGAGAGAAAGCTGCTGT 3951
Qy 3913 GCAAGACTAGAGAAAGCCCTTGAAGAACCCGATCGAGCTCGGTCCGCGGAGGAA 3972
Db 3952 GCAGAGCTAGAGAAAGCCCTTGAAGAACCCGATCGAGCTCGGTCCGCGGAGGAA 4011
Qy 3973 GGTGCTCCACCGGAAAGCAAGCAACCAACCAATCAAGCCAGCCACCGCGAGGACG 4032
Db 4012 GGTGCTCCACCGGAAAGCAAGCAACCAACCAATCAAGCCAGCCACCGCGAGGACG 4071
Qy 4033 CAGATCGCAATGTCGCGCATCGTGGGTGCGCAGAGCACAGCCAGTGCATGAGCCTG 4092
Db 4072 CAGATCGCAATGTCGCGCATCGTGGGTGCGCAGAGCACAGCCAGTGCATGAGCCTG 4131
Qy 4093 CTGGCTCCGCGCATCGAGCGGAGAAAGATTTCAACTCCAGAGAAATTTAGTGGGCT 4152
Db 4132 CTGGCTCCGCGCATCGAGCGGAGAAAGATTTCAACTCCAGAGAAATTTAGTGGGCT 4191

OY	4153	CTTAAAGAACGCATGCAACCCAAATATTCCTCAACCAATTAAGATGAGCATGAAACATGCA	4212
Db	4192	CTTAAAGAAAGCATGCAACCAATATTCCTCAACCAATTAAGATGAGCATGAAACATGCA	4251
OY	4213	GCCAAAGATGTGCTGTGTCTGTGATACCGTGCACTTTGGAAGCCAGGCATCCAAATGT	4272
Db	4252	GCCAAAGATGTGCTGTGTCTGTGATACCGTGCACTTTGGAAGCCAGGCATCCAAATGT	4311
OY	4273	CTCGAATGTCAAGTGAATGTGTCAACCCCAATGCTTCAACGTGCTTTGGCAAGCATGCGGCG	4332
Db	4312	CTCGAATGTCAAGTGAATGTGTCAACCCCAATGCTTCAACGTGCTTTGGCAAGCATGCGGCG	4371
OY	4333	TTGCTGTGTGAATATGTGCAACAACCTTCAACGAGGCTTCTGCCGTGAACAAATGAATCC	4392
Db	4372	TTGCTGTGTGAATATGTGCAACAACCTTCAACGAGGCTTCTGCCGTGAACAAATGAATCC	4431
OY	4393	CCAGTGTCTCAAGCAACGAAGGCCCAAGACGATCTTGCACTTGAAGAGTGTGAATGAGTG	4452
Db	4432	CCAGTGTCTCAAGCAACGAAGGCCCAAGACGATCTTGCACTTGAAGAGTGTGAATGAGTG	4491
OY	4453	CCCGAATTAACAACGAGGACAGCAAGGCTGGGACGAAAGTACATTTGTCTTGAGAGGA	4512
Db	4492	CCCGAATTAACAACGAGGACAGCAAGGCTGGGACGAAAGTACATTTGTCTTGAGAGGA	4551
OY	4513	TCAAAAGTCTCATTTATGACAAATGAAACGACAGACCTGGAACGAGGCTGGTGAAGAA	4572
Db	4552	TCAAAAGTCTCATTTATGACAAATGAAACGACAGACCTGGAACGAGGCTGGTGAAGAA	4611
OY	4573	TTTGAAGCTGTGCTTTCCGACGAGGAGTATCTATTTATGATGTGCGTGTGTGCTCCGAA	4632
Db	4612	TTTGAAGCTGTGCTTTCCGACGAGGAGTATCTATTTATGATGTGCGTGTGTGCTCCGAA	4671
OY	4633	CTCGCAATTAAGCCCAAGCA-----	4653
Db	4672	CTCGCAATTAAGCCCAAGCAAGATGTCCATACATGAAAGATGAATCTCACCCGAC	4731
OY	4654	-----	4653
Db	4732	AACAACCTGTGACCCGAGGAACCTCTTACTTGCTAGCTCCAGCTTCCCTGACAAACAG	4791
OY	4654	-----	4654
Db	4792	CGCTGGGTCAACCGCTTGAATCAAGTTGTGCGAGGTGGAGAGTTCTTAAGGAAAAAGCA	4851
OY	4663	GAAAGTGAATGCTAAACGTGCTTGGAACCTCCCTGCTGAAACGTGGAAGGTGAATGAACGGCTA	4722
Db	4852	GAAAGTGAATGCTAAACGTGCTTGGAACCTCCCTGCTGAAACGTGGAAGGTGAATGAACGGCTA	4911
OY	4723	GACATGAATGCAACCTGCGCTTCAAGTACACAGGTGTGTGTGTGGGACCCGAGGAAGGG	4782
Db	4912	GACATGAATGCAACCTGCGCTTCAAGTACACAGGTGTGTGTGTGGGACCCGAGGAAGGG	4971
OY	4783	CTCTACGCCCTGAATGTCTTGAAAACTCCCTTAACCAATGTCACAGGAATTTGAGCAAGTC	4842
Db	4972	CTCTACGCCCTGAATGTCTTGAAAACTCCCTTAACCAATGTCACAGGAATTTGAGCAAGTC	5031
OY	4843	TTTCCAAATTTAATTAATCAAGGACCTGGAAGAACTCATGATGTGACGAGAGAAAGCGG	4902
Db	5032	TTTCCAAATTTAATTAATCAAGGACCTGGAAGAACTCATGATGTGACGAGAGAAAGCGG	5091
OY	4903	GCACTGTGTCTTGTGACGTGGAAGAAAGTGAACAGTCCCTGGGCCAGTCCCACTGCTCT	4962
Db	5092	GCACTGTGTCTTGTGACGTGGAAGAAAGTGAACAGTCCCTGGGCCAGTCCCACTGCTCT	5151
OY	4963	GCCCAAGCCGCAATCTCAACCAACATTTTGAAGCTGTCAAGGGCTGCACTTGTTTGGG	5022
Db	5152	GCCCAAGCCGCAATCTCAACCAACATTTTGAAGCTGTCAAGGGCTGCACTTGTTTGGG	5211
OY	5023	GCAGGCAAGATTGAGAAAGGGGCTCTGCACTGTGAGCAATGCCACGACAAAGTGTCTATT	5082
Db	5212	GCAGGCAAGATTGAGAAAGGGGCTCTGCACTGTGAGCAATGCCACGACAAAGTGTCTATT	5271
OY	5083	CTCCGCTACACGAAACCTCAAGCAATATCTGCACTCCGAAAAAGATAGACCTCAAG	5142

Db	5272	CTCCGCTACACGAAACCTCAGCAATACCTGCATCCGGAAGAAAGATAGAGACCTCGAG	5331
Oy	5143	CCCTGAGCGTGTATCCACTTCAACCAATTACATCTCTCATTTGGAAACCAATAAATTCTAC	5202
Db	5332	CCCTGAGCGTGTATCCACTTCAACCAATTACATCTCTCATTTGGAAACCAATAAATTCTAC	5391
Oy	5203	GAATTCGACATGAAAGCAGTACAGCCTGAGGAAATCTCGATAGATGACATTCCTTG	5262
Db	5392	GAATTCGACATGAAAGCAGTACAGCCTGAGGAAATCTCGATAGATGACATTCCTTG	5451
Oy	5263	GCACCTGCTGTGTGTGCGCCTCTTTCACACACTTCCCTGTCTCATCTGTGCGAGTGAAC	5322
Db	5452	GCACCTGCTGTGTGTGCGCCTCTTTCACACACTTCCCTGTCTCATCTGTGCGAGTGAAC	5511
Oy	5333	AGCGGAGGGCAGCGAGAGAGTACTTGTGTGTTTCCACGAATTGGAGTTCGTGAT	5382
Db	5512	AGCGGAGGGCAGCGAGAGAGTACTTGTGTGTTTCCACGAATTGGAGTTCGTGAT	5571
Oy	5383	TCTTACGGAACGTAAGCCGACAGACGATCTCAATGAGTCTGACTTACCTTTGGCCTTT	5442
Db	5572	TCTTACGGAACGTAAGCCGACAGACGATCTCAATGAGTCTGACTTACCTTTGGCCTTT	5631
Oy	5443	GCTTACAGAGAACCTCTATCTGTGTTGTGACCACTTCAACTCATCTGAAATTTGAGATC	5502
Db	5632	GCTTACAGAGAACCTCTATCTGTGTTGTGACCACTTCAACTCATCTGAAATTTGAGATC	5691
Oy	5503	CAGGACGCTCTCTGACGAGGGACCCCTGCCGAGCGTACCTGACATCCCGAACCCCGGC	5562
Db	5692	CAGGACGCTCTCTGACGAGGGACCCCTGCCGAGCGTACCTGACATCCCGAACCCCGGC	5751
Oy	5563	TACTGTGGCCCTGCCATTTCTCAGAGACGATTTACTTGGCGTCTCATATCCAGATTTAA	5622
Db	5752	TACTGTGGCCCTGCCATTTCTCAGAGACGATTTACTTGGCGTCTCATATCCAGATTTAA	5811
Oy	5623	TTTAAAGGTTCATTTGCTGCAAGGGAACCTCGTAAAGAGTCCGGGACTGAAACCAACCGG	5682
Db	5812	TTTAAAGGTTCATTTGCTGCAAGGGAACCTCGTAAAGAGTCCGGGACTGAAACCAACCGG	5871
Oy	5683	GGCCCGTTCACCTCCCGACGACGCCCAACAAGCGAGGCCCAACCACTGTAACAAGACAC	5742
Db	5872	GGCCCGTTCACCTCCCGACGACGCCCAACAAGCGAGGCCCAACCACTGTAACAAGACAC	5931
Oy	5743	ATTCACAAAGCGGTGGCTTCAGACCCAGCGCGCCGGAAGGCCCAGGCAACCCGAGAG	5802
Db	5932	ATTCACAAAGCGGTGGCTTCAGACCCAGCGCGCCGGAAGGCCCAGGCAACCCGAGAG	5992
Oy	5803	CCAAAGCACACCCACCGCTACCGCGAGGGGGGAGCCGAGCTTGGCGAGGACAACTCTCT	5862
Db	5992	CCAAAGCACACCCACCGCTACCGCGAGGGGGGAGCCGAGCTTGGCGAGGACAACTCTCT	6051
Oy	5863	GGCCCGCCCCCTGGAGCGAGAAAGTCCCCCGCCCGAGTCTCAGACCGCGGAGAGCGG	5922
Db	6052	GGCCCGCCCCCTGGAGCGAGAAAGTCCCCCGCCCGAGTCTCAGACCGCGGAGAGCGG	6111
Oy	5923	TCCCGCGGAGGCGTGTTTGAAGACAGCAGCAGGGGCGGCTGCTGCGGAGCCGTGAG	5983
Db	6112	TCCCGCGGAGGCGTGTTTGAAGACAGCAGCAGGGGCGGCTGCTGCGGAGCCGTGAG	6172
Oy	5983	ACCCGCGTGTCCAGGTGAACAAGGAGAGGGGAGAGTGCCTCTCAAGTTTTCACGGTT	6041
Db	6172	ACCCGCGTGTCCAGGTGAACAAGGAGAGGGGAGAGTGCCTCTCAAGTTTTCACGGTT	6231
Oy	6043	AACACTGTCACTTAATTAT 6060	
Db	6232	AAAACCAACTCTCATCT 6249	

RESULT 7
US-10-618-941-1
; Sequence 1, Application US/106189411
; Publication No. US20040197792A1
; GENERAL INFORMATION:

APPLICANT: WHITE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: CAENEPEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 8656
TYPE: DNA
ORGANISM: Homo sapiens
US-10-618-941-1

Query Match 86.2%; Score 5669.8; DB 18; Length 8656;
Best Local Similarity 95.5%; Pred. No. 0;
Matches 5978; Conservative 0; Mismatches 37; Indels 246; Gaps 4;

QY 1 AGAGCCGCCAGTGGGAGATGTTGAAGTTCAAAATGAGACCGGGAATCCTTTGATGCT 60
DB 33 AGAGCCGCCAGTGGGAGATGTTGAAGTTCAAAATGAGACCGGGAATCCTTTGATGCT 92
QY 61 GGTGCTGTCGAACCCATTGCGACCGGGCCTCCAGCTGTAATCTTTCTCCAGGGGAAA 120
DB 93 GGTGCTGTCGAACCCATTGCGACCGGGCCTCCAGCTGTAATCTTTCTCCAGGGGAAA 152
QY 121 CCACCTTTATGACTCAACAGAGATGTCCTCTTTCCGAGAGAGGATATTAGATGCC 180
DB 153 CCACCTTTATGACTCAACAGAGATGTCCTCTTTCCGAGAGAGGATATTAGATGCC 212
QY 181 CTCTTTGTTCTCTTTGAAGATSCAGTCAAGCTGCTCTGATGAAGATTAAAGCAGTGA 240
DB 213 CTCTTTGTTCTCTTTGAAGATSCAGTCAAGCTGCTCTGATGAAGATTAAAGCAGTGA 272
QY 241 AACTTTGTCGGAA---GTATTCGACACCATAGCTGATGAAGAGGCTCCAGCTTGC 297
DB 273 AACTTTGTCGGAAAGTGTATTCGACACCATAGCTGATGAAGAGGCTCCAGCTTGC 332
QY 298 GCATAAGACTTCGAAGTCAAGAGTCTTGTAGTTGTGTCATCTTCTGTAAGTCAAGTTC 357
DB 333 GCATAAGACTTCGAAGTCAAGAGTCTTGTAGTTGTGTCATCTTCTGTAAGTCAAGTTC 392
QY 358 GTAAAGAGAAAGCAACCGGGAATCTATGCTATGAAGATGAAGAAAGGCTTTA 417
DB 393 GTAAAGAGAAAGCAACCGGGAATCTATGCTATGAAGATGAAGAAAGGCTTTA 452
QY 418 TTGGCCCAAGAGAGTTCATTTTTTGAAGAAAGCGGAACATATTATCTCGAAGACA 477
DB 453 TTGGCCCAAGAGAGTTCATTTTTTGAAGAAAGCGGAACATATTATCTCGAAGACA 512
QY 478 AGCCCTGATCCCCCAATTACAGTATGCTTTCAAGACAAATAACCTTTATCTGATG 537
DB 513 AGCCCTGATCCCCCAATTACAGTATGCTTTCAAGACAAATAACCTTTATCTGATG 572
QY 538 GAGAAATATCAGCTGAGGGGACTTGCTGTCACTTTGAATGATATGAGACCAATTA 597
DB 573 ATGAAATATCAGCTGAGGGGACTTGCTGTCACTTTGAATGATATGAGACCAATTA 632
QY 598 GATGAAAACCTGATTAAGTTTACCTTACAGTATGCTTTGCTGCTGTTCAAGCTTCAT 657
DB 633 GATGAAAACCTGATTAAGTTTACCTTACAGTATGCTTTGCTGCTGTTCAAGCTTCAT 692
QY 658 CTGATGGGATACCTGATCGAGACATCAAGCTGAGAACATTTCTGTTGACCGACAGGA 717
DB 693 CTGATGGGATACCTGATCGAGACATCAAGCTGAGAACATTTCTGTTGACCGACAGGA 752
QY 718 CACATCAAGCTGTGATTTTGGATCTGCGCGAAAATGAATTTCAACAAGATGTGAAT 777
DB 753 CACATCAAGCTGTGATTTTGGATCTGCGCGAAAATGAATTTCAACAAGATGTGAAT 812

QY 778 GCCAACTCCGATTTGGAGCCCAAGATTACATGCTCTGAAGTGTGATGATGAAC 837
DB 813 GCCAACTCCGATTTGGAGCCCAAGATTACATGCTCTGAAGTGTGATGATGAAC 872
QY 838 GGGGATGAAAAAGCACTACGGCTGGAATGATGATGATGATGATGATGATGATGATGAT 897
DB 873 GGGGATGAAAAAGCACTACGGCTGGAATGATGATGATGATGATGATGATGATGATGAT 932
QY 898 TATGAGATGATTTATGAGGAGATCCCTCTCGAGAGGAACTCTGCCGAACCTTCAAT 957
DB 933 TATGAGATGATTTATGAGGAGATCCCTCTCGAGAGGAACTCTGCCGAACCTTCAAT 992
QY 958 AACATTATGAATTTCCAGCGGTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAC 1017
DB 993 AACATTATGAATTTCCAGCGGTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAC 1052
QY 1018 TTTCTTGATCTGAATTCAAAGCTTTGTCGGCCAGAAAAGAGACTGAAGTTGAAGT 1077
DB 1053 TTTCTTGATCTGAATTCAAAGCTTTGTCGGCCAGAAAAGAGACTGAAGTTGAAGT 1112
QY 1078 CTTTGCTGCAATCTTTCTTCTTAATAATTGACTGGAACAATCTGTAATCTCTCCC 1137
DB 1113 CTTTGCTGCAATCTTTCTTCTTAATAATTGACTGGAACAATCTGTAATCTCTCCC 1172
QY 1138 CCTTGCTCCAGCCCTCAAGTCTGACATGACACTCCCAATTTTGATGAACAGAGAG 1197
DB 1173 CCTTGCTCCAGCCCTCAAGTCTGACATGACACTCCCAATTTTGATGAACAGAGAG 1232
QY 1198 AATTGCTGGGTTTCAATCTCTCCGTCAGTGAAGCCCTCAGGCTTCTCGGATGAAGA 1257
DB 1233 AATTGCTGGGTTTCAATCTCTCCGTCAGTGAAGCCCTCAGGCTTCTCGGATGAAGA 1292
QY 1258 CTGCGCTTTGCGGTTTCTGTAAGCAAGCACTGCGGATTTCTGTAATCTGATG 1317
DB 1293 CTGCGCTTTGCGGTTTCTGTAAGCAAGCACTGCGGATTTCTGTAATCTGATG 1352
QY 1318 GTTGTGCGGATCTGGAATCCCTGCGCAAGCACTAGCTCCAGTGAAGAACTTCTCATC 1377
DB 1353 GTTGTGCGGATCTGGAATCCCTGCGCAAGCACTAGCTCCAGTGAAGAACTTCTCATC 1412
QY 1378 AAAAGCAAGACTCAAGACTCTCAGCAAGCAAGTCTCAAGATGAGAGCAAGAAATGACC 1437
DB 1413 AAAAGCAAGACTCAAGACTCTCAGCAAGCAAGTCTCAAGATGAGAGCAAGAAATGACC 1472
QY 1438 CGGTTACATCGAGAGTCTCAAGTCTGAGTCTGCTTATGTCAGAAAGTGTGAGCTG 1497
DB 1473 CGGTTACATCGAGAGTCTCAAGTCTGAGTCTGCTTATGTCAGAAAGTGTGAGCTG 1532
QY 1498 AAGGCTCTGAGACTCAGAGATCCCTCTGAGAGAGAACCTTGCTACCTACATCAAGAA 1557
DB 1533 AAGGCTCTGAGACTCAGAGATCCCTCTGAGAGAGAACCTTGCTACCTACATCAAGAA 1592
QY 1558 TGCAGTACCTTAAAGCAAGTTTGAGCAAGCAAGATGAGTGTCCAGAGAGATGAC 1617
DB 1593 TGCAGTACCTTAAAGCAAGTTTGAGCAAGCAAGATGAGTGTCCAGAGAGATGAC 1652
QY 1618 AAAAGCACTGACCTTCTCATATATTCAGAGAGCAAGCCGGAAGCTTCAAGAAATCAAA 1677
DB 1653 AAAAGCACTGACCTTCTCATATATTCAGAGAGCAAGCCGGAAGCTTCAAGAAATCAAA 1712
QY 1678 GAGCAGAGATACAGGCTCAAGTGAAGAAATGAGTGTGATGATGATGATGATGATGATG 1737
DB 1713 GAGCAGAGATACAGGCTCAAGTGAAGAAATGAGTGTGATGATGATGATGATGATGATG 1772
QY 1738 GATCTTGTCTCAGCAAGAGAGAGTCTCTAAGATCTGAGCTGAGAGAGTCTCGG 1797
DB 1773 GATCTTGTCTCAGCAAGAGAGAGTCTCTAAGATCTGAGCTGAGAGAGTCTCGG 1832
QY 1798 CTTGCTGCTGAAGAAATTCAGCGGAAAGCAGAGATGTCAGCATTAATCTGTTGAAGCT 1857
DB 1833 CTTGCTGCTGAAGAAATTCAGCGGAAAGCAGAGATGTCAGCATTAATCTGTTGAAGCT 1892
QY 1858 AAGGATCAAGGAGAGCTGGAATGTGGGAGAAATGAGAACTGAGAGATGTAATCTGAG 1917

1893 AAGGATCAAGGGAGCCCTGAAGTGGAGAAATATCCGAAACTGGAGAAATCAATCTGAG 1952
QY 1918 CAGAGCTCAAAATTCAGAGCTCCAAAGAACTGAGAGGCT-----1962
Db 1953 CAGAGCTCAAAATTCAGAGCTCCAAAGAACTGAGAAAGGCTGPAAGGCAAGCAGC 2012
QY 1963 -----GCAAGAGAGGAGCCCGAGAGAGGCTG 1989
Db 2013 GAGGCCACCGAGCTGCTGAGAAATATCCCGAGCAAGAGCGAGCCGAGAGGAGCTG 2072
QY 1990 GAGAGCTGCAAGAACGAGAGATTCCTTCTGAAGGCTATCAGAAAGAGCTGTGGAAGCT 2049
Db 2073 GAGAGCTGCAAGAACGAGAGATTCCTTCTGAAGGCTATCAGAAAGAGCTGTGGAAGCT 2132
QY 2050 GAGGAGCGGCGCAATTCCTGAGAACAGATTAAGACTTAAGACATATGAGCCGTAGA 2109
Db 2133 GAGGAGCGGCGCAATTCCTGAGAACAGATTAAGACTTAAGACATATGAGCCGTAGA 2192
QY 2110 GAAAAAGAGCTGAAGATGACATCCAGACAAAAATCCCAAGATCCAGAGATGAGCTGAT 2169
Db 2193 GAAAAAGAGCTGAAGATGACATCCAGACAAAAATCCCAAGATCCAGAGATGAGCTGAT 2252
QY 2170 AAAATTCGAGCTCGAAGAGAAACATCGGAGGCCCAAGTCTCAGCCGACCTAGAA 2229
Db 2253 AAAATTCGAGCTCGAAGAGAAACATCGGAGGCCCAAGTCTCAGCCGACCTAGAA 2312
QY 2230 GTGCACCTGAAAAGAGAGGAGGAGCACTATGAGAGAAAGATTAAGTGTGGACAATCG 2289
Db 2313 GTGCACCTGAAAAGAGAGGAGGAGCACTATGAGAGAAAGATTAAGTGTGGACAATCG 2372
QY 2290 ATTAAGAAAGAGCTGCTGCTGCAAGAGAGACATGAGAGCATATGAGAGACACAGAGAG 2349
Db 2373 ATTAAGAAAGAGCTGCTGCTGCAAGAGAGACATATGAGAGACACAGAGAG 2432
QY 2350 GAGGCCCAAGAGAGGAGGAGAAATTCCTCAGGAAACAGAGGCCATGATCAATGCTATGAT 2409
Db 2433 GAGGCCCAAGAGAGGAGGAGAAATTCCTCAGGAAACAGAGGCCATGATCAATGCTATGAT 2492
QY 2410 TCCAGAGTCAAGTCCCTGAGAACAGAGATTTGTGAACTGTCTGAAAGCCAAATTAACCTGCA 2469
Db 2493 TCCAGAGTCAAGTCCCTGAGAACAGAGATTTGTGAACTGTCTGAAAGCCAAATTAACCTGCA 2552
QY 2470 GCAAAATAGCAATCTTTTACCCAAAGAAACATGAAGGCCCAAGAGAGATGATTTCTGAA 2529
Db 2553 GCAAAATAGCAATCTTTTACCCAAAGAAACATGAAGGCCCAAGAGAGATGATTTCTGAA 2612
QY 2530 CTCAAGCAACAGAAATTTTACCTGAGAACAGAGCTGAGAGTTGAGAGCCCAAGACCGA 2589
Db 2613 CTCAAGCAACAGAAATTTTACCTGAGAACAGAGCTGAGAGTTGAGAGCCCAAGACCGA 2672
QY 2590 AAACTGAGAGAGCACTGAGAGAGATTCAGCCACCAAGACCAACATGAGAGAGATGAGCTG 2649
Db 2673 AAACTGAGAGAGCACTGAGAGAGATTCAGCCACCAAGACCAACATGAGATGAGCTG 2732
QY 2650 CTGGAATCTGAGAGCAAGATTTGCGGAGAGTCAATGATGAGACAGAGAGCAAGAACTGAG 2709
Db 2733 CTGGAATCTGAGAGCAAGATTTGCGGAGAGTCAATGATGAGACAGAGAGCAAGAACTGAG 2792
QY 2710 CTCAAGCCAGAGCTCAAGAGCTACAGCTCTCCCTGAGAGAGCCGAGATTCACATGTCACA 2769
Db 2793 CTCAAGCCAGAGCTCAAGAGCTACAGCTCTCCCTGAGAGAGCCGAGATTCACATGTCACA 2852
QY 2770 GCCCTGAGAGCTGACCGGCGGCGCTGAGAGAGCCAGCTTCGCCAGGCGAAGACAGAGCTG 2829
Db 2853 GCCCTGAGAGCTGACCGGCGGCGCTGAGAGAGCCAGCTTCGCCAGGCGAAGACAGAGCTG 2912
QY 2830 GAAAGAGCAACAGAGAGAGCTGGAAGAGATTCAGGCACTCAACGCGCATATGAGATGAA 2889
Db 2913 GAAAGAGCAACAGAGAGAGCTGGAAGAGATTCAGGCACTCAACGCGCATATGAGATGAA 2972
QY 2890 ATCCAGCGCAAAATTTGATGCTCTTCGTAAAGAGCTGTACTGTAAACAGACCTTGAAGAG 2949

Db 2973 ATCCAGCGCAAAATTTGATGCTCTTCGTAAAGAGCTGTACTGTAAACAGACCTGAGAGAG 3032
QY 2950 CAGCTAAACAGAGCTACCGAGAGCAACGCTGAACTCAACCAACAAATCTTACTGTTCC 3009
Db 3033 CAGCTAAACAGAGCTACCGAGAGCAACGCTGAACTCAACCAACAAATCTTACTGTTCC 3092
QY 3010 AAAACAATCTGATGAGGCTTCTGCGCCCAACGAGAGATTTGAACATCTCGAGATGAGAGT 3069
Db 3093 AAAACAATCTGATGAGGCTTCTGCGCCCAACGAGATTTGAACATCTCGAGATGAGAGT 3152
QY 3070 GACCAATCCCGCGGAGAGATCAACGAGAGATGAGCTTACCAAGCCAGAAAGCAACG 3129
Db 3153 GACCAATCCCGCGGAGAGATCAACGAGAGATGAGCTTACCAAGCCAGAAAGCAACG 3212
QY 3130 ATGAGAGCTCTGAAAGACCAAGTGCACATGCTGAGAGAACAGTCAATGATTTGGAGGCC 3189
Db 3213 ATGAGAGCTCTGAAAGACCAAGTGCACATGCTGAGAGAACAGTCAATGATTTGGAGGCC 3272
QY 3190 CTAAACGATGAGCTGCTGAAAAGAGCGGCAATGAGAGGCGCTGAGAGAGCGTCTGGGT 3249
Db 3273 CTAAACGATGAGCTGCTGAAAAGAGCGGCAATGAGAGGCGCTGAGAGAGCGTCTGGGT 3332
QY 3250 GATGAGAAATCCCAATTTGAGATGAGTCCGAGTTGAGAGAGCTGAGAGAAATGCTGAGACCGAG 3309
Db 3333 GATGAGAAATCCCAATTTGAGATGAGTCCGAGTTGAGAGAGCTGAGAGAAATGCTGAGACCGAG 3392
QY 3310 AAAAGAGCAGGCGGAGAGCCGATCAAGCGATCAACGAGTCTGCCAGTGTGAGAGCTG 3369
Db 3393 AAAAGAGCAGGCGGAGAGCCGATCAAGCGATCAACGAGTCTGCCAGTGTGAGAGCTG 3452
QY 3370 GCAGTGAAGGAGCAACAGGCTGAGATTCGCTCTGAGAGAGGCTTCAAGAGACAGAG 3429
Db 3453 GCAGTGAAGGAGCAACAGGCTGAGATTCGCTCTGAGAGAGGCTTCAAGAGAGCAAG 3512
QY 3430 CTGAAGGCGGAGAGCTCTCTGACAGACTCAATGAGCTGAGAGAGAGATGCTATGCTT 3489
Db 3513 CTGAAGGCGGAGAGCTCTCTGACAGACTCAATGAGCTGAGAGAGAGATGCTATGCTT 3572
QY 3490 GAAATGAATGCCCGAAGCTTACAGCAGAGCTGAGAGCTGAACGAGAGCTCAACAGAGG 3549
Db 3573 GAAATGAATGCCCGAAGCTTACAGCAGAGCTGAGAGCTGAACGAGAGCTCAACAGAGG 3632
QY 3550 CTTCTGGAAGAGCAAGCCAAATTAACAGCAGAGTGAACCTGCAAGAAATTCACATTTTC 3609
Db 3633 CTTCTGGAAGAGCAAGCCAAATTAACAGCAGAGTGAACCTGCAAGAAATTCACATTTTC 3692
QY 3610 CGTCTGACTCAAGAGCTGCAAGAGAGCTCTAGATCGGCTGATCTACTGAAGACAGAAAG 3669
Db 3693 CGTCTGACTCAAGAGCTGCAAGAGAGCTCTAGATCGGCTGATCTACTGAAGACAGAAAG 3752
QY 3670 AGTGAATTTGAGATGATCAGCTGAGAAACATTCAGGTTCTTATTCCTGAAAGGTGAAA 3729
Db 3753 AGTGAATTTGAGATGATCAGCTGAGAAACATTCAGGTTCTTATTCCTGAAAGGTGAAA 3812
QY 3730 ATGGAAGGCACTATTTCTCAACAAACCAATCTATGATTTTCTGCAAGCCAAATGAGAC 3789
Db 3813 ATGGAAGGCACTATTTCTCAACAAACCAATCTATGATTTTCTGCAAGCCAAATGAGAC 3872
QY 3790 CAACCTGCTAATAAGAAAGAGGTTTATTTAGTCAGAGAAAGAGACCTGCTTTAACCC 3849
Db 3873 CAACCTGCTAATAAGAAAGGTTTATTTAGTCAGAGAAAGAGACCTGCTTTAACCC 3891
QY 3850 ACAAGGTTCTCTGAGATGACATGAGCTGAGAGCTGAGAGAGAGAGAGAGAGCTCCG 3909
Db 3892 ----AGGTTCTCTGAGATGACATGAGCTGAGAGCTGAGAGAGAGAGAGAGAGCTCCG 3947
QY 3910 TGTGAGAGCTGAGAGAGAGGCTTCAAGAGACCCGATGAGAGCTCGGCTCCGCGGAGAG 3969
Db 3948 TGTGAGAGCTGAGAGAGAGGCTTCAAGAGAGCCGATGAGAGCTCGGCTCCGCGGAGAG 4007
QY 3970 GAAAGTCCCAACGCAAGCAAGAGCAACCAACCAATTCACAGGCAAGCCAGCGAGAG 4029
Db 4008 GAAAGTCCCAACGCAAGCAAGAGCAACCAACCAATTCACAGGCAAGCCAGCGAGAG 4067

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4068 CAGAGATGGCAATGTCGGCATGTCGGGTCGCAAGACCAAGCCAGTGCATGAGC 4127
4090 CTGCTGCCCCCGCATTCAGCCGAGAAAGAGTCTTCACTCCAGAGAAATTTAGTCG 4149
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4150 CGTCTTAAGAACGCAATGCAACCAATATTTCTCAACGATTTCAACGTAAGCATG 4209
4188 CGTCTTAAGAACGCAATGCAACCAATATTTCTCAACGATTTCAACGTAAGCATG 4247
4210 CGAGCCACAAAGT 4269
4248 CGAGCCACAAAGT 4307
4270 TGTCTGAATGTGAGGTGATGTGTCAACCCAGTGTCTCAAGTGTCTTGCAGCCACTGC 4329
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4330 GGTGTGCTGTGTAATATGTCACCACTTCAACGAGGCTTGTGCGGTGAACAATGAC 4389
4368 GGTGTGCTGTGTAATATGTCACCACTTCAACGAGGCTTGTGCGGTGAACAATGAC 4427
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4450 GTGCCAGAAATTAACAAACGAGACGAGGCTGAGGACGAGAGTCAATTTGCTGTGAG 4509
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4548 GGTTCAAAAGTCTCTCAATTTATGACAAATGAAACGAGAGACTGACAGAGCGGTGAA 4607
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4668 GAATCTGCAAAATACAGCCAAAGCAATGTCCTCATATCTGAAGATGAAATCTCACCG 4727
4654 ----- 4653
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4654 -----GAAAA 4659
4788 CAGCGCTGGGTCAACGCTTGAATCAGTTGTGCAAGTGGAGAGTTTCTAGGAAAAA 4847
4660 GCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4719
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4908 CTAGACATGAATGCAACGCTGCTTCAAGTACCAAGTGTGTGTGTGTGTGTGTGTGTGT 4967
4780 GGGCTCTAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4839
4968 GGGCTCTAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5027
4840 GTCTTCAAAATTAATATTAATCAAGACCTGAGAGGCTACTCAATGATGAGAGAGAG 4899
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5088 CGGACCTGT 5147

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5148 CTGCCCCAGCCGACATCTCACCAATTTTTGAAGCTGTCAAGGGCTGCCACTGTGTT 5207
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5208 GGGGACGAGAGATTGAGAACGGGCTGTGATCTGTGACAGCCATGCCCCAGAAAGTGTG 5267
5080 ATTCTCCGCTACACGAAAACTCAGCAAAATCTGATCTCCGAGAGAGATGAGACTCA 5139
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5200 TAGAAATGCAATGAGAGAGTACAGCTCGAGAAATTCCTGATTAAGATGACATTTCC 5259
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5260 TTGGCAGCTGT 5319
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5680 CGGGGCGGCTTCCAGAGAGAGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5739
5868 CGGGGCGGCTTCCAGAGAGAGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5927
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5800 GAGCCAGACACCCCAACGCTTACGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5859
5988 GAGCCAGACACCCCAACGCTTACGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6047
5860 CCGGCGCGGCTTCCAGAGAGAGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5919
6048 CCGGCGCGGCTTCCAGAGAGAGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6107
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6108 CCGTCCCCCGGAGAGGCTGTTTGAAGACAGACAGAGGAGGAGGAGGAGGAGGAGGAGG 6167
5980 AGGACCCGCTGTCCAGAGTAAACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6039
6168 AGGACCCGCTGTCCAGAGTAAACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6227
6040 GTTAAACATGTCACTATTAAT 6060

Db 6228 AGAAAAACAACCTCTCATCT 6248

RESULT 8
US-10-028-946-1
; Sequence 1, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanhuan
; APPLICANT: Miranda, Maricar
; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: Lex-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-1

Query Match 86.1%; Score 5661.4; DB 13; Length 6165;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 16; Indels 243; Gaps 3;

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QY 79 GCCAGCGGGCCCTCCAGGCTGAATCTGTCTTCCAGGGGAAACACCCCTTTATGACTCA 138
Db 61 GCCAGCGGGCCCTCCAGGCTGAATCTGTCTTCCAGGGGAAACACCCCTTTATGACTCA 120

QY 139 CAGCAGATGTCTCTCTTCCGAGAGGGAATTTAGATGCCCTTTGTTCTCTTTGAA 198
Db 121 CAGCAGATGTCTCTCTTCCGAGAGGGAATTTAGATGCCCTCTTTGTTCTCTTTGAA 180

QY 199 GAATGAGTCAAGCTGCTCTGATGAAGATTAAAGCAGTGAACAATTGTCGGAGAT 258
Db 181 GAATGAGTCAAGCTGCTCTGATGAAGATTAAAGCAGTGAACAATTGTCGGAGAT 240

QY 259 TCCGACACCATAGCTGATTTACAGAGCTCCAGGCTTGGCAAGAATTGCAAGTCA 318
Db 241 TCCGACACCATAGCTGATTTACAGAGCTCCAGGCTTGGCAAGAATTGCAAGTCA 300

QY 319 AGTCTTTAGTGTGTGCTCACTTTGCTGAAGTGAAGTGTGAAGAGAAACAACCGG 378
Db 301 AGTCTTTAGTGTGTGCTCACTTTGCTGAAGTGAAGTGTGAAGAGAAACAACCGG 360

QY 379 GACATCTAGTATGAAAGTGAAGAAAGAGGCTTTATTTGGCCAGAGCAAGTTTCA 438
Db 361 GACATCTAGTATGAAAGTGAAGAAAGAGGCTTTATTTGGCCAGAGCAAGTTTCA 420

QY 439 TTTTGTGAAGAGAGCGGAACATATTATCTGAAGCAACAAGCCGTGATCCCAATTA 498
Db 421 TTTTGTGAAGAGAGCGGAACATATTATCTGAAGCAACAAGCCGTGATCCCAATTA 480

QY 499 CAGTATGCTCTTCAAGACAAAATACCTTTATCTGATGAAGAAATATCAGCTGAGAG 558
Db 481 CAGTATGCTCTTCAAGACAAAATACCTTTATCTGATGAAGAAATATCAGCTGAGAG 540

QY 559 GACTTGCTGTCACTTTGATATGATAGAGCAAGTTATGAAATACCTGATACGTTT 618
Db 541 GACTTGCTGTCACTTTGATATGATAGAGCAAGTTATGAAATACCTGATACGTTT 600

QY 619 TACCTAGTGAAGTATTTGGCTGTCAAGAGCTTCATGTAGGAGTACGATGAGA 678
Db 601 TACCTAGTGAAGTATTTGGCTGTTCACAGCGTTTCACTGATGAGATACGATGAGA 660

QY 679 GACATCAAGCTGAGAACTTCTGTTGACCGCAGAGACATCATCAAGCTGTGATTTT 738
Db 661 GACATCAAGCTGAGAACTTCTGTTGACCGCAGAGACATCATCAAGCTGTGATTTT 720

QY 739 GGATCGCCGGAATAATGAAATTTCAACAAGATGTGAAATGCCAACTCCGATTTGGAGC 798
Db 721 GGATCGCCGGAATAATGAAATTTCAACAAGATGTGAAATGCCAACTCCGATTTGGAGC 780

QY 799 CCAGATTACATGCTCTGAAAGTGTGACTGATGAACGGGAGATGAAAAAGGACCTTAC 858
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QY 859 GGCCTGACTGACTGTGTGCTCACTGAGGCGCTGATTTGCTATGAGATATTTATGGAGA 918
Db 841 GGCCTGACTGACTGTGTGCTCACTGAGGCGCTGATTTGCTATGAGATATTTATGGAGA 900

QY 919 TCCCCCTTCGAGAGGAACTTGGCCGAACCTTCAATTAATTTATTTTCCAGCGG 978
Db 901 TCCCCCTTCGAGAGGAACTTGGCCGAACCTTCAATTAATTTATTTTCCAGCGG 960

QY 979 TTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTTCTGATCTGATCAAAAGC 1038
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QY 1039 TTGTTGTCGGCCGCAAAAAGAGACTGAAGTTGAAGTCTTTGCTGCTATCTTTCTTC 1098
Db 1021 TTGTTGTCGGCCGCAAAAAGAGACTGAAGTTGAAGTCTTTGCTGCTATCTTTCTTC 1080

QY 1099 TCTAAATTTGACTGGAACCAATTCGTACTCTCTCCCTCGTTTCCCAACCTCAAG 1158
Db 1081 TCTAAATTTGACTGGAACCAATTCGTACTCTCTCCCTCGTTTCCCAACCTCAAG 1140

QY 1159 TCTGAGATGACACCTTCATTTTGAATGAACAGAGAAAGATTTGTGGTTTCACTCTCT 1218
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QY 1219 CCGTGCAGCTGAACCCCTCAAGGCTTCCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG 1278
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QY 1279 TACAGCAAGGACTGGGGAATCTTGTGATGATCTGAGTCTGTGTGTGCGGCTTGAAGCTCC 1338
Db 1261 TACAGCAAGGACTGGGGAATCTTGTGATGATCTGAGTCTGTGTGTGCGGCTTGAAGCTCC 1320

QY 1339 CTTGCAAGACTAGCTCAATGGAAGAAAGAACTTCTATCAAAAGCAAAAGCTTACAAGAC 1398
Db 1321 CTTGCAAGACTAGCTCAATGGAAGAAAGAACTTCTATCAAAAGCAAAAGCTTACAAGAC 1380

QY 1399 TCTCAGGACAAAGTGTCACAAGATGGAAGAGAAATGACCCGGTTTACATGGAGAGTCTCA 1458
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QY 1459 GAGGTGAGGCTGTGCTTACTGAAAGAGTGAAGCTGAAGGCTTCTGAGACTCAGAGA 1518
Db 1441 GAGGTGAGGCTGTGCTTACTGAAAGAGTGAAGGCTTCTGAGACTCAGAGA 1500

QY 1519 TCCCTCTGAGAGAGGACTTGTCTTACTCATCAAGATGCAAGTACTTAAAGCGAAGT 1578
Db 1501 TCCCTCTGAGAGAGGACTTGTCTTACTCATCAAGATGCAAGTACTTAAAGCGAAGT 1560

QY 1579 TTGAGCAACACGAGATGAGAGTGTCCAGAGAGATGACAAACACTGACGCTTCCAT 1638
Db 1561 TTGAGCAACACGAGATGAGAGTGTCCAGAGAGATGACAAACACTGACGCTTCCAT 1620

QY 1639 GATATCAGAGACAGAGCTCGGAAGCTTCAAGAAATCAAAAGAGAGAGTACAGGCTCAA 1698
Db 1621 GATATCAGAGACAGAGCTCGGAAGCTTCAAGAAATCAAAAGAGAGAGTACAGGCTCAA 1680

QY 1699 GTGGAAGAAATGAGTGAATGATGAATCACTTGGAGAGAGATTTGTCTCAGAGAAAGA 1758
Db 1681 GTGGAAGAAATGAGTGAATGATGAATCACTTGGAGAGAGATTTGTCTCAGAGAAAGA 1740

QY	1759	CGGATGATCTCTTAAGAACTCGAGCTGAGAGAGTCTCGGCTTCTGCTGAAGAAATTCAAG	1818
Db	1741	CGGATGATCTCTTAAGAACTCGAGCTGAGAGAGTCTCGGCTTCTGCTGAAGAAATTCAAG	1800
QY	1819	CGGAAGCGACAGAAATGTACGATTAACCTGTGAAGCTTAAGGATCAAGGGAGGCTGAA	1878
Db	1801	CGGAAGCGACAGAAATGTACGATTAACCTGTGAAGCTTAAGGATCAAGGGAGGCTGAA	1860
QY	1879	GTGGAGAAATATGCGAAACTGAGAGAGATCAATGCTGAGCAGACCTCAAAATTCAGAG	1938
Db	1861	GTGGAGAAATATGCGAAACTGAGAGAGATCAATGCTGAGCAGACCTCAAAATTCAGAG	1920
QY	1939	CTCCAAAGGAAACTGAGAGAGCT-----	1962
Db	1921	CTCCAAAGGAAACTGAGAGAGCTTTAAAGCAGACGAGGCCACCGAGCTGCTCAG	1980
QY	1963	-----GCAAGAGGAGAGCTCGAGAGGAGCTGGAAGCTTCAGAACCGAGAG	2010
Db	1981	AATATCCGCGAGGCAAAAGAGGAGCTCGAGAGGAGCTGGAAGCTTCAGAACCGAGAG	2040
QY	2011	GATTTCTTGAAGGCGATCAGAAAGAGCTGTGAGAGCTGAGAAACGCGGCATTTCTG	2070
Db	2041	GATTTCTTGAAGGCGATCAGAAAGAGCTGTGAGAGCTGAGAAACGCGGCATTTCTG	2100
QY	2071	GAGAAACAAGGTAAAGAGACTAGAGACCTATGAGCCTAAGAAACAACCTAGAGATGAC	2130
Db	2101	GAGAAACAAGGTAAAGAGACTAGAGACCTATGAGCCTAAGAAACAACCTAGAGATGAC	2160
QY	2131	ATCCGACAAAAATCCCAACAGATCCAGAGATGCGTGTAAAAATTCCTGAGACTGGAAG	2190
Db	2161	ATCCGACAAAAATCCCAACAGATCCAGAGATGCGTGTAAAAATTCCTGAGACTGGAAG	2220
QY	2191	AAACATCGGAGGCGCCCAAGTCTCAGGCCGAGCACCTAGAGAGTGCACTTGAAACAGAAAG	2250
Db	2221	AAACATCGGAGGCGCCCAAGTCTCAGGCCGAGCACCTAGAGAGTGCACTTGAAACAGAAAG	2280
QY	2251	CAGCACTATGAGAAAGATTAAAGTTTGGACAATCAATTAAGAAAGACTCGGCTGAC	2310
Db	2281	CAGCACTATGAGAAAGATTAAAGTTTGGACAATCAATTAAGAAAGACTCGGCTGAC	2340
QY	2311	AAGGAGACACTGAGAGACATGATGAGAGACACGAGGAGGAGGCCATGAGAAAGGCGAA	2370
Db	2341	AAGGAGACACTGAGAGACATGATGAGAGACACGAGGAGGAGGCCATGAGAAAGGCGAA	2400
QY	2371	ATTCTCAGCGAAACAGAAAGCGCATGATCATCTATGAGATTCCAGATCAGATCCCTGAA	2430
Db	2401	ATTCTCAGCGAAACAGAAAGCGCATGATCATCTATGAGATTCCAGATCAGATCCCTGAA	2460
QY	2431	CAGAGGATTTGTGAACTGTCTGAAAGCCAAATAAATTGACGAATAATGACGCTTTTAAAC	2490
Db	2461	CAGAGGATTTGTGAACTGTCTGAAAGCCAAATAAATTGACGAATAATGACGCTTTTAAAC	2520
QY	2491	CAAAAGAAACATGAAGGCCCAAGAAAGATGATTTCTGAACTCAGGCAACAGAAATTTTAC	2550
Db	2521	CAAAAGAAACATGAAGGCCCAAGAAAGATGATTTCTGAACTCAGGCAACAGAAATTTTAC	2580
QY	2551	CTGAGAGACACAGGCTGAGAGGCTTGAAGGCCCAAGAACCGAAACTGAGAGACAGCTGGAG	2610
Db	2581	CTGAGAGACACAGGCTGAGAGGCTTGAAGGCCCAAGAACCGAAACTGAGAGACAGCTGGAG	2640
QY	2611	AAGATCAGCCACCAAGACCAACGTGACAAAGATGCGGCTGTGAACTTGAGACAAAGATTG	2670
Db	2641	AAGATCAGCCACCAAGACCAACGTGACAAAGATGCGGCTGTGAACTTGAGACAAAGATTG	2700
QY	2671	CGGAGAGTCAAGTCTGAGACAAGAGAGCAAGAACTGAGAGCTTCAGGCGCAGCTCAAGAG	2730
Db	2701	CGGAGAGTCAAGTCTGAGACAAGAGAGCAAGAACTGAGAGCTTCAGGCGCAGCTCAAGAG	2760
QY	2731	CTACAGCTCTCCCTGACGAGAGCGCAAGTCAACAGTTGACAGCCCTGACAGGCTGCACGGGCG	2790
Db	2761	CTACAGCTCTCCCTGACGAGAGCGCAAGTCAACAGTTGACAGCCCTGACAGGCTGCACGGGCG	2820
QY	2791	GCCCTGAGAGGCAAGCTTCCGCGAGCGAAGACAGAGCTTGAGAGAGACCAACAGCAAGACT	2850

Db	2821	GGCTTGGAGACCAAGCTTCCGACGCGAGACAGAGCTGGAGAGACCAACGCGAAAGCT	2880
QY	2851	GAAGAGAGATCCAGGCACTCACGGCACTAGAGATGMAATCCAGCGCAATTTGATGCT	2910
Db	2881	GAAGAGAGATCCAGGCACTCACGGCACTAGAGATGMAATCCAGCGCAATTTGATGCT	2940
QY	2911	CTTGCTAATCAGCTGTACTGTATATCAACAGACTTGAGAGACAGCTTAAACAGCTGACCGAG	2970
Db	2941	CTTGCTAATCAGCTGTACTGTATATCAACAGACTTGAGAGACAGCTTAAACAGCTGACCGAG	3000
QY	2971	GACAAAGCTGAATCCAAACAAACCTTCACTTGTCCAAACAACTCGATGAGGCTTCT	3030
Db	3001	GACAAAGCTGAATCCAAACAAACCTTCACTTGTCCAAACAACTCGATGAGGCTTCT	3060
QY	3031	GGCGCCAAACGACGAGATTGTACAACCTGCGAAGTGAATGAGACACTTCCGCGCGAGATC	3090
Db	3061	GGCGCCAAACGACGAGATTGTACAACCTGCGAAGTGAATGAGACACTTCCGCGCGAGATC	3120
QY	3091	ACGGAGCAGAGATGACAGCTTACAGCCAGAGCAAAAGATGAGGCTCTGAGACCAACG	3150
Db	3121	ACGGAGCAGAGATGACAGCTTACAGCCAGAGCAAAAGATGAGGCTCTGAGACCAACG	3180
QY	3151	TGCACCAATGCTGAGAGGAACAGSTCAATGATTTGGAGGCCCTTAAACGATGAGCTGTGAA	3210
Db	3181	TGCACCAATGCTGAGAGGAACAGSTCAATGATTTGGAGGCCCTTAAACGATGAGCTGTGAA	3240
QY	3211	AAAGAGCGGCAAGTGGAGGAGCTTGAGAGGACGCTCGTGGGTGATGAGAAATCCCAATTGAG	3270
Db	3241	AAAGAGCGGCAAGTGGAGGAGCTTGAGAGGAGCTCTTGGGTGAATGAGAAATCCCAATTGAG	3300
QY	3271	TGTCGGGTTTCAGAGCTGACAGAGATGCTGGAACAACGAGAAACAGACAGGCGAGAGCC	3330
Db	3301	TGTCGGGTTTCAGAGCTGACAGAGATGCTGGAACAACGAGAAACAGACAGGCGAGAGCC	3360
QY	3331	GATCAGCGGATCACCCAGCTCTGCGCAGGTGATGAGCTGCGCACTGAAAGAGCAAAAGGCT	3390
Db	3361	GATCAGCGGATCACCCAGCTCTGCGCAGGTGATGAGCTGCGCACTGAAAGAGCAAAAGGCT	3420
QY	3391	GAGATTCTCGCTGACAGCAGGCTCTGAAAGAGAGAGCTGAGGCCGAGAGGCTCTCT	3450
Db	3421	GAGATTCTCGCTGACAGCAGGCTCTGAAAGAGAGAGCTGAGAGGCCGAGAGGCTCTCT	3480
QY	3451	GACAAAGCTCAATGACCTGAGAGAGAGCAATGCTATGCTTGAATGAAATGCCGAGGCTTA	3510
Db	3481	GACAAAGCTCAATGACCTGAGAGAGAGCAATGCTATGCTTGAATGAAATGCCGAGGCTTA	3540
QY	3511	CAGCAGAAAGCTGAGAGCTGAAACGAGAGCTCAACAGAGGCTTCTGGAAGAGCAAGCCAA	3570
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QY	3571	TTACAGCAGCAGATGAGACCTGACAGAAAATCACTTTCCGTGCACTCAAGAGACTGCA	3630
Db	3601	TTACAGCAGCAGATGAGACCTGACAGAAAATCACTTTCCGTGCACTCAAGAGACTGCA	3660
QY	3631	GAAAGCTTAGATCGGGCTGATCTTACTGAAACAGAAAGAGTGAATGAGAGGCACTAATTTCTCA	3690
Db	3661	GAAAGCTTAGATCGGGCTGATCTTACTGAAACAGAAAGAGTGAATGAGAGGCACTAATTTCTCA	3720
QY	3691	GAAGAACTTCAAGGTTCTCTATTTCTCATGAAAAGGTGAAAATGAAAGGCACTAATTTCTCA	3750
Db	3721	GAAGAACTTCAAGGTTCTCTATTTCTCATGAAAAGGTGAAAATGAAAGGCACTAATTTCTCA	3780
QY	3751	CAAAACCAAACTCATTTGATTTCTGCAAGCCCAAAATGAGCAACCTGCTTAAAGAAAAG	3810
Db	3781	CAAAACCAAACTCATTTGATTTCTGCAAGCCCAAAATGAGCAACCTGCTTAAAGAAAAG--	3838
QY	3811	GGTTATTTAGTCGACGGAAAGAGACCTGCTTAAACCAACAGGTTCTCTGACAGTAC	3870
Db	3839	-----AGTTCTCTGCAATAC	3855
QY	3871	AATGAGCTGAAGCTGGCCCTGAGAGAGAGAAAGCTGCTGTGACAGCTTAGAGAAAGCC	3930

Dh 3856 AATGAGCTGAAGCTGGCCCTGAGAGAGAGAAAAGCTGCTGTGCAAGACTGAGAGAACCC 3915
Qy 3931 CTTTCAAGAGACCCGCGATTCGAGCTCCGGTCCGCCGAGAGAGCTGCCACCGCAAGACGCA 3990
Db 3916 CTTTCAAGAGACCCGCGATTCGAGCTCCGGTCCGCCGAGAGAGAGCTGCCACCGCAAGACGCA 3975
Qy 3991 ACGGACCAACCCACACCATCCTCAGCGGACCGGACGAGAGAGAGATTCGCAATGTCGCCGCC 4050
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Qy 4051 ATGCTGCGGTCCGCAAGACGCAAGCCCATGTCATGAGCTGTGGCCCGCCATCCAGC 4110
Db 4036 ATGCTGCGGTCCGCAAGACGCAAGCCCATGTCATGAGCTGTGGCCCGCCATCCAGC 4095
Qy 4111 CGGAGAAAGAGTCTTCACTCAGAGAGATTTTATGTCGCGCTTTAAGGAAAGCATGCAAC 4170
Db 4096 CGGAGAAAGAGTCTTCACTCAGAGAGATTTTATGTCGCGCTTTAAGGAAAGCATGCAAC 4155
Qy 4171 CACAAATATTCTTCACCGATTCAACGTAAGACTGAGAGCCCAAAAGTGTGCTG 4230
Db 4156 CACAAATATTCTTCACCGATTCAACGTAAGACTGAGAGCCCAAAAGTGTGCTG 4215
Qy 4231 TGTCTGATATCCGTGCACTTTGGACGCGCATTCGCAATGTCGATGTCAGTGATG 4290
Db 4216 TGTCTGATATCCGTGCACTTTGGACGCGCATTCGCAATGTCGATGTCAGTGATG 4275
Qy 4291 TGTCAACCCAGAGTCCCAAGTCCGCTTGGACGCGCATTCGCGGCTTGTGCTGATATG 4350
Db 4276 TGTCAACCCAGAGTCCCAAGTCCGCTTGGACGCGCATTCGCGGCTTGTGCTGATATG 4335
Qy 4351 AACACATTGACCGAGGCTTTCGCGCTGCAAAAATGAACTCCCAAGGTCTCCAGACGAG 4410
Db 4336 AACACATTGACCGAGGCTTTCGCGCTGCAAAAATGAACTCCCAAGGTCTCCAGACGAG 4395
Qy 4411 GAGCCGACGACGACTTGGACCTGGAAGGCTGATGAGTCCGCAATTAACAAACGA 4470
Db 4396 GAGCCGACGACGACTTGGACCTGGAAGGCTGATGAGTCCGCAATTAACAAACGA 4455
Qy 4471 GGAAGCAAGGCTGGGACGAGAGATCATTTGCTGGAGGATCAAAATCTCTCATTTAT 4530
Db 4456 GGAAGCAAGGCTGGGACGAGAGATCATTTGCTGGAGGATCAAAATCTCTCATTTAT 4515
Qy 4531 GACAAATGAAGCAGAGAGCTGACAGAGCCGCTGAGAGATTTGAGCTGTGCCCTTCCC 4590
Db 4516 GACAAATGAAGCAGAGAGCTGACAGAGCCGCTGAGAGATTTGAGCTGTGCCCTTCCC 4575
Qy 4591 GACGCGGATGTAATTAATTAATGTCGCTTGGTGTCTTCCGAACTGCAAAATACGCCAA 4650
Db 4576 GACGCGGATGTAATTAATTAATGTCGCTTGGTGTCTTCCGAACTGCAAAATACGCCAA 4635
Qy 4651 GCA----- 4653
Db 4636 GGAAGATGTCCTAATCAATCACTGAAGATGCAATCTCACCGGACACCACTGCTGGCCGAG 4695
Qy 4654 ----- 4653
Db 4636 AGAACCTCTCTACTTGCTAGCTCCAGGCTTCCCTGCAAAAGCGGTGGGTCAACGCTTAA 4755
Qy 4654 -----GAAAAAGCAGAGCTGATGCTAACTG 4680
Db 4756 GAATCAATGTTGTCGAGGTGGAGAGTTCCTAGGAGAAAAAGCAGAGCTGATGCTAACTG 4815
Qy 4681 CTTGAGAACTCCTGCTGAAACTGGAAGGTATGACCGTCTAGACATGAACTGACGCGCTG 4740
Db 4816 CTTGAGAACTCCTGCTGAAACTGGAAGGTATGACCGTCTAGACATGAACTGACGCGCTG 4875
Qy 4741 CCCTTCAATGACGAGGTGTGTTGGTGGGACCGAGAGAGGCTCTACGCTGCAATGTC 4800
Db 4876 CCCTTCAATGACGAGGTGTGTTGGTGGGACCGAGAGAGGCTCTACGCTGCAATGTC 4935
Qy 4801 TTGAGAAATCCTCCTTAACCATATGTCAGAGAAATTTGAGAGCTTCTCAAAATTTATATTC 4860
Db 4936 TTGAGAAATCCTCCTTAACCATATGTCAGAGAAATTTGAGAGCTTCTCAAAATTTATATTC 4995

Qy 4861 AAGACCTGAGAGCTACTCATGATAGCAGAGAGAGCGGGCACTGTGCTTGTGAC 4920
Db 4996 AAGACCTGAGAGCTACTCATGATAGCAGAGAGAGCGGGCACTGTGCTTGTGAC 5055
Qy 4921 GTGAAGAAAGTAAACAGTCCCTGGCCAGTCCACCTGCTGGCCAGCCGACATCTCA 4980
Db 5056 GTGAAGAAAGTAAACAGTCCCTGGCCAGTCCACCTGCTGGCCAGCCGACATCTCA 5115
Qy 4981 CCCAATTTTGAAGCTGTCAAGGGCTGCCACTGTTTGGGGGAGGCAAGTTAGAAC 5040
Db 5116 CCCAATTTTGAAGCTGTCAAGGGCTGCCACTGTTTGGGGGAGGCAAGTTAGAAC 5175
Qy 5041 GGGCTTCATCTGTGACGCAATGCCAGCAAAAGTGTATTCCTCGCTACACGAAAC 5100
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Db 5236 CTCAGCAAAATCTGATCCGAAAGAGATAGAGACTCAGAGCCCTGACGCTGATCCAC 5295
Qy 5161 TTCACCAATTCAGATCTCATTTGGAACCAATAAATCTACGAAATGACATGAAGAG 5220
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Qy 5221 TACAGCTCGAGAAATCTGATAGAGATGCAATTCCTTGGACCTGTGTGTTGCC 5280
Db 5356 TACAGCTCGAGAAATCTGATAGAGATGCAATTCCTTGGACCTGTGTGTTGCC 5415
Qy 5281 GCTCTTCGCAAGCTTCCCTGTCTCAATCGTGAAGGTGAACAGCGAGGGCAGCGAGAG 5340
Db 5416 GCTCTTCGCAAGCTTCCCTGTCTCAATCGTGAAGGTGAACAGCGAGGGCAGCGAGAG 5475
Qy 5341 GAGTACTTGTGTGTTTCAAGAAATTTGAGTGTGTCGATTTCTTACGGAAGAGTATG 5400
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Qy 5461 CTGTTTGTGACCCCACTTCACTCACTGAAATTAATGAGTCAAGGACGCTCTCCAGCA 5520
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Qy 5521 GGAACCCCTGCGAGGCTACTGGAATTCGGAACCCGCGCTTACTTGGGCCCTGCCATT 5580
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Db 5776 AAGGAAACCTGTAAGAGAGTCCGAGCTGGAACCAACCGGGGCCGCTCCACTCCGCG 5835
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QY 5941 GAAGACGACGACGAGGCGGCTGCTGCGGAGCCGTGAGAGCCCGCTGTCCAGGTG 6000
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QY 6001 AACAAAGGGAAGAGGCGAGAGTGC 6023
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RESULT 9

US-10-791-666-1
; Sequence 1, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fiddie, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PASTESEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-791-666-1

Query Match 86.1%; Score 5661.4; DB 18; Length 6165;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 16; Indels 243; Gaps 3;

QY 19 ATCTTAATTTCAAAATATGAGGCGGGAATCTTTGAGTCTGTCTGTGAACCAT 78
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Db 1 ATGTTAAAGTTCAAAATATGAGGCGGGAATCTTTGAGTCTGTCTGTGAACCAT 60
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QY 79 GCCAGCGGCGGCTCCAGAGCTGAATCTGTTCTCCAGGGAACCAACCTTTATGACTCA 138
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Db 61 GCCAGCGGCGGCTCCAGAGCTGAATCTGTTCTCCAGGGAACCAACCTTTATGACTCA 120
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QY 139 CAGCAGATGTCTCTCTTTCCGAGAAAGGATATAGATGCCCTCTTGTCTTTGAA 198
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Db 121 CAGCAGATGTCTCTCTTTCCGAGAAAGGATATAGATGCCCTCTTGTCTTTGAA 180
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QY 199 GAATGACGTACGCTCTCTCTGATGAAGATTAGACAGTGAACCTTTGTCCGAAGTAT 258
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Db 181 GAATGACGTACGCTCTCTCTGATGAAGATTAGACAGTGAACCTTTGTCCGAAGTAT 240
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QY 259 TCCGACACCATAGCTAGTTAGAGAGCTCCAGCTTCCGCAAGGACTTCCAGTCA 318
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Db 241 TCCGACACCATAGCTAGTTAGAGAGCTCCAGCTTCCGCAAGGACTTCCAGTCA 300
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QY 319 AGTCTTGAAGTGTGTGTCACTTTGCTGAAGTGCAGGTGTGAAGAGAAAGCAACCG 378
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Db 301 AGTCTTGAAGTGTGTGTCACTTTGCTGAAGTGCAGGTGTGAAGAGAAAGCAACCG 360
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QY 379 GACATTTATGCTATGAAGTGAAGAAAGGCTTTATTTGGCCGAGAGAGGTTTCA 438
| | | | |
Db 361 GACATTTATGCTATGAAGTGAAGAAAGGCTTTATTTGGCCGAGAGAGGTTTCA 420
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QY 439 TTTTGAAGGAAGAGGGAACATATTATCTGAAGACCAAGCCGTGATCCCAATTA 498
| | | | |
Db 421 TTTTGAAGGAAGAGGGAACATATTATCTGAAGACCAAGCCGTGATCCCAATTA 480
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QY 499 CAGTATGCTTTTCAGACAAATACTTTATCTGATGAGGAATATCAGCTTGAAG 558
| | | | |
Db 481 CAGTATGCTTTTCAGACAAATACTTTATCTGATGAGGAATATCAGCTTGAAG 540
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QY 559 GACTTGCTGCACTTTTGAATAGATATGAGACCAAGTATGATGAAAACCTGATACAGTT 618
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| | | | |
Db 601 TACCTAGCTGACCTGATTTTGGCTGTTCAAGCGTTTCATCTGATGGATACGTGATCGA 660
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QY 679 GACATCAAGCTTGAGAACCTTCTCGTTGACCCGACAGACATCAAGCTGTGATTTT 738
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Db 661 GACATCAAGCTTGAGAACCTTCTCGTTGACCCGACAGACATCAAGCTGTGATTTT 720
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QY 739 GGAATCGCGCGGAAAATGAATTCAAACAAGATGTGAATGCCAACTCCCGATTTGGAGCC 798
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Db 721 GGAATCGCGCGGAAAATGAATTCAAACAAGATGTGAATGCCAACTCCCGATTTGGAGCC 780
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QY 799 CCAGATTATCATGCTCTCTGAGTGTGATGATGAAGAGGAGATGAAAAGGACCTTAC 858
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QY 859 GGCCTGACTGCTGACTGTGTGCTGAGTGGCGCTGATTTGCTATGAGATGATTTATGGAGA 918
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QY 919 TCCCCCTTGCGAGAGGAACTCTGCGAGAACCTTCAATTAATGAAATTTCCAGCGG 978
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QY 1039 TTGTTGTCGCGCGCAAGAAAGAGTGAAGTGAAGTCTTTCTTGAATTCGAATTC 1098
| | | | |
Db 1021 TTGTTGTCGCGCGCAAGAAAGAGTGAAGTGAAGTCTTTCTTGAATTCGAATTC 1080
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Db 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGATGAAGAACTCCGTTGTGGGTTTTCG 1260
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QY 1279 TACAGCAAGGCACTGGGATTTCTGGTGAATCTGAGTCTGTGTCTGGGTCTGACCTCC 1338
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| | | | |
Db 1381 TCTCAAGACATGCTCAACAAGTGAAGCAAGAAATGACCCGGTTACATCGAGAGTGTCA 1440
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Db 1441 GAGGTGAGAGCTGTCTTATGATGAAGAGAGTGAAGCTGAAGCCCTGAGACTGAGAGA 1500
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QY 1519 TCCCTCTGAGACAGGACCTTCTCACTATCATCAGAAATGCAATGAGTTAAAGGAAAGT 1578
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Db 1501 TCCCTCTGAGACAGGACCTTCTCACTATCATCAGAAATGCAATGAGTTAAAGGAAAGT 1560
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QY 1579 TTGAGCAAGACAGATGAGAGTGTCCAGAGAGATGACAAAGCACTGAGCTTCCAT 1638
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Db 1561 TTGAGCAAGACAGATGAGAGTGTCCAGAGAGATGACAAAGCACTGAGCTTCCAT 1620
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QY 1639 GATATTCAGAGACAGAGCCGGAAGCTCCAGAAATTCAAAGACAGAGATACAGAGCTCA 1698
| | | | |

Db 1621 GATATCAGAGACGAGCCGGAGCTCCAGAAATCAAAGACGAGATCCAGGCTCAA 1680
QY 1699 GTGGAGAAATGAGGTTGATGATGAATCAGTTGGAAAGAGATTTTGTCTCAGCAAGA 1758
Db 1681 GTGGAGAAATGAGGTTGATGATGAATCAGTTGGAAAGAGATTTTGTCTCAGCAAGA 1740
QY 1759 CGAGTGTATCTCTACGAATCTGAGTGAAGAGTCTCGGCTTGCTGTAAGAAATTCAG 1818
Db 1741 CGAGTGTATCTCTACGAATCTGAGTGAAGAGTCTCGGCTTGCTGTAAGAAATTCAG 1800
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Db 1801 CGAAAGCCACAGATGTGACATAAATCTTTGAAGCTTAAGATCAAGGAAGCTTGA 1860
QY 1879 GTGGAGAAATGAGGTTGATGATGAATCAGTTGGAAAGAGATTTTGTCTCAGCAAGA 1938
Db 1861 GTGGAGAAATGAGGTTGATGATGAATCAGTTGGAAAGAGATTTTGTCTCAGCAAGA 1920
QY 1939 CTCGAAGAAACTGAGAAAGGCT----- 1962
Db 1921 CTCGAAGAAACTGAGAAAGGCTTTAAAGCCAGACGGAAGCCACGAGCTGCTCAG 1980
QY 1963 -----GCAAGAGCGAGCCGAGAGGAGCTGAGAAAGCTGCAAGACCGAGAG 2010
Db 1981 AATATCCGCGAGCAAGAGAGCGAGCCGAGAGGAGCTGAGAAAGCTGCAAGACCGAGAG 2040
QY 2011 GATTCCTTGAAGGCTCAAGAAAGAGCTGTGTGAAGCTGAGAAAGCCGCCATTTCTTG 2070
Db 2041 GATTCCTTGAAGGCTCAAGAAAGAGCTGTGTGAAGCTGAGAAAGCCGCCATTTCTTG 2100
QY 2071 GAGAACAAAGTAAAGACTAGAGACCTAGAGCCGTAGAGAAACAGACTGAAGATGAC 2130
Db 2101 GAGAACAAAGTAAAGACTAGAGACCTAGAGCCGTAGAGAAACAGACTGAAGATGAC 2160
QY 2131 ATCCAGACAAATATCCACAGATCCAGAGATGGCTGATTAATTTCTGAGCTCGAAGAG 2190
Db 2161 ATCCAGACAAATATCCACAGATCCAGAGATGGCTGATTAATTTCTGAGCTCGAAGAG 2220
QY 2191 AAAACATCGGAGAGCCCAAGTCTCAGCCCGACACTAGAGTGCCTGAAACAGAAAGAG 2250
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Db 2281 CAGCACTATGAGAAAGATTAAGTGTGACAAATCAGATTAAGAAAGACCTGAGTGCAC 2340
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QY 2371 ATTCTCAGGGAACAGAGGCGATGATCAATGCTATGAGATTTCCAAATCGATCCCTGGA 2430
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Db 2581 CTGAGAGACAGAGCTGGGAAGTTGAGGCGCCAGAAACCGAAACCTGAGAGAGAGCTGAG 2640
QY 2611 AAGATCAGCCACCAAGACCAAGTGAAGTCCGCTGCTGGAACCTGAGACCAAGATTG 2670
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QY 2671 CGGAGGTCAGTCTTGAGACGAGAGAGCAAACTGAGCTCAAGCCGCTCAAGAG 2730

Db 2701 CGGAGGTCAGTCTTGAGACGAGAGAGCAAACTGAGCTCAAGCCGCTCAAGAG 2760
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Db 2761 CTACAGCTCTCCCTGAGAGAGCGCAAGTCAAGTTGAAGCTTCAGAGCTTCACAGGCG 2820
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QY 2851 GAAAGAGAGATCCAGGCACTCAGGCACTAGAGATGAATTCAGCGCAAAATTTGATGCT 2910
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QY 3031 GGCAGCAACGACGAGATTTGACAACTGCAAGTGAAGTGAACATCTCCGCGGAGATC 3090
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QY 3091 ACGGAACGAGATTCAGCTTACAGCCAGAAAGCAACAGATGAGGCTCTGAACCAAG 3150
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QY 3751 CAAACCAATCTATTGATTTTCTGCAAGCCAAATGAGCAACCTGCTTAAGAAAG 3810
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QY 3811 GGTATTTATGTCGACGGAAGAAGACCTGCTTTACCAACAGGTTCTCTGCAGTAC 3870
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QY 3871 AATGAGCTGAAGCTGSCCTCTGAGAGAGAAAGCTCGCTGTGACAGAGCTAGAGAAAGCC 3930
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DB 3916 CTTTCAAGAACCCGCAATCGAGCTCCGGTCCGCCGGGAGAAAGCTGCCAACCAGAAAGCA 3975
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DB 4576 GACGGGAGATGATCTATTCATGAGTGCCTGTTGCTTCCGAATCCGAATTAAGCCAA 4635
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DB 4636 GCAAGATGTCCCATACATCTGAAGATGGAATCTCACCCGACACACTGTGCCCCGGG 4695
QY 4654 ----- 4653
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US-09-964-956-10
/ Sequence 10, Application US/09964956
/ Publication No. US20040043926A1
/ GENERAL INFORMATION:
/ APPLICANT: Gerlach, Valerie L
/ APPLICANT: MacDougall, John R
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Stone, David
/ APPLICANT: Gunther, Erik
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Grose, William M
/ APPLICANT: Alsodbrook II, John P
/ APPLICANT: Lepley, Denise M
/ APPLICANT: Burgess, Catherine B
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Kethuda, Ramesh
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Leach, Martin D
/ APPLICANT: Shinkels, Richard A
/ TITLE OF INVENTION: No. US20040043926A1e1 Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-124
/ CURRENT APPLICATION NUMBER: US/09/964,956
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 60/235,631
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/235,633
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/235,808
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/236,064
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/236,065
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/236,066
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/237,434
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: 60/237,434
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/238,321
/ PRIOR FILING DATE: 2000-10-05
/ PRIOR APPLICATION NUMBER: 60/238,399
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 60/238,396
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 60/276,667
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/294,823
/ PRIOR FILING DATE: 2001-05-31
/ PRIOR APPLICATION NUMBER: 60/304,868
/ PRIOR FILING DATE: 2001-07-12
/ NUMBER OF SEQ ID NOS: 127
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 10
/ LENGTH: 6189
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ORGANISM: Homo sapiens
US-09-964-956-10
Query Match 85.7% Score 5631; DB 11; Length 6189;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 45; Indels 246; Gaps 4;

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      5281  GCCTTCCAAAGAGTTCCTGCTGATTCGATTCGAGTGAACGCGCAGGCGAGAGAG 5340
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      5341  GAGTACTTCTGCTGTTTCCAGAAATTTGAGTGTGAGATTCCTTACGGAAGACCTAGC 5400
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      5533  CGCAGACGATCTCAAGTGAAGTGCCTTACCTTTGACCTTTCACAGAAACCTTAT 5592
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      5593  CTGTTGTGACCACTTCAATCTGATTCGAGTGAATTCAGAGCAAGCTTCTGAGCA 5652
      5521  GGGACCCCTGCGGAGCGTACCTGACATCCCGAACCCGCGCTACCTGGCCCTGACAT 5580
      5653  GGGACCCCTGCGGAGCGTACCTGACATCCCGAACCCGCGCTACCTGGCCCTGACAT 5712
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RESULT 11

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US-10-262-511-1
; Sequence 1, Application US/10262511
; Publication No. US2004003823A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millett, Isabelle
; APPLICANT: Beyman, John A.
; APPLICANT: Kexuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Paturajan, Meera

```

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; APPLICANT: Spylek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellemann, Karen
; APPLICANT: Malyanek, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zeinhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Bergins, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT FILING DATE: 2003-05-28
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 1
; LENGTH: 6189
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(6159)
US-10-262-511-1
Query Match      85.7%; Score 5631; DB 17; Length 6189;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 45; Indels 246; Gaps 4;

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 Db 4453 GGAACGAAGGCTGGAGCAGAAAGTACATTTGCTGAGAGGATCAAAAGTCTCATTTAT 4512

OY	453	GACAAATGAAGCCAGAGAAACCTGACACAGAGCCGGTGGAAAGAAATTTGACCTGCTTCC	4530
Db	4513	GACAAATGAAGCCAGAGAAACCTGACACAGAGCCGGTGGAAAGAAATTTGACCTGCTTCC	45722
OY	4591	GACGGGAGATGATCTAATTCATGGTGGCGGTGGTCTCGAACTGCAGAAATACAGCCAA	4650
Db	4573	GACGGGAGATGATCTAATTCATGGTGGCGGTGGTCTCGAACTGCAGAAATACAGCCAA	4652
OY	4651	GCA-----	4653
Db	4633	GCAGATGTCCTCAATACATCTGAAGATGCAATCTCACCGCACACCACTGCTGGCCGGG	4692
OY	4654	-----	4653
Db	4693	AGAACCTCTACTGTGCTAGCTCCAGCTTCCCTGCAAAACAGCGTGGGTACCGCCTTA	4752
OY	4654	-----GAAAAAGCAAGACTGATGCTAAACTG	4680
Db	4753	GAATCAGTTTGCCAGAGTGGAGAGATTTCTAGGGGAAAAAGCAAGCTGATGCTAACTG	4812
OY	4681	CTTGGAAATCTCCCTGCTGTAACCTGGAAGGTATGACCGCTAGACATGAACTTGACGCTG	4740
Db	4813	CTTGGAAATCTCCCTGCTGTAACCTGGAAGGTATGACCGCTAGACATGAACTTGACGCTG	4872
OY	4741	CCCTTCAGTACCAAGTGGTGGTGGGACCGAGAAAGGCTCTACGCGCTGAATGTC	4800
Db	4873	CCCTTCAGTACCAAGTGGTGGTGGGACCGAGAAAGGCTCTACGCGCTGAATGTC	4932
OY	4801	TTGAAAACTCCCTTACCCCATATGCCAGAAATTTGAGAGATCTTCCAAATTTATATATC	4860
Db	4933	TTGAAAACTCCCTTACCCCATATGCCAGAAATTTGAGAGATCTTCCAAATTTATATATC	4992
OY	4861	AAAGACCTGAGAAAGCTACTCATGATATGACAGAAAGACGGGACATGTGCTTGTGGAC	4920
Db	4993	AAAGACCTGAGAAAGCTACTCATGATATGACAGAAAGACGGGACATGTGCTTGTGGAC	5052
OY	4921	GTGAAGAAAGTGAACATGCTCCCTGGCCCAATGCCACTGCTGCCACGCCGACATTTCA	4980
Db	5053	GTGAAGAAAGTGAACATGCTCCCTGGCCCAATGCCACTGCTGCCACGCCGACATTTCA	5112
OY	4981	CCCAACATTTTGAAGCTGTCAAGGGGCTGCCACTGTTTGGGGCAGGCAAGATTGAGAAC	5040
Db	5113	CCCAACATTTTGAAGCTGTCAAGGGGCTGCCACTGTTTGGGGCAGGCAAGATTGAGAAC	5172
OY	5041	GGGCTCTGCAATCTGTGACAGCCATGCCACGCAAAATGCTCATTTCTCGCTACAGAAAC	5100
Db	5173	GGGCTCTGCAATCTGTGACAGCCATGCCACGCAAAATGCTCATTTCTCGCTACAGAAAC	5232
OY	5101	CTCAGCAAAATCTGCATCCGGAAGAGATGAGACCTCAGAGCCCTGCACTGATATCCAC	5160
Db	5233	CTCAGCAAAATCTGCATCCGGAAGAGATGAGACCTCAGAGCCCTGCACTGATATCCAC	5292
OY	5161	TTCAACCAATTAACGATATCTCATTTGGAACCAATTAATTTCTACGAAATCGACATGAACAG	5220
Db	5293	TTCAACCAATTAACGATATCTCATTTGGAACCAATTAATTTCTACGAAATCGACATGAACAG	5352
OY	5221	TACAGCGCTCGAGGAATTCGGAATAAAGACCAATTCCTTTGCACTGCTGTGTTGGC	5280
Db	5353	TACAGCGCTCGAGGAATTCGGAATAAAGACCAATTCCTTTGCACTGCTGTGTTGGC	5412
OY	5281	GCTCTTTCACACAGCTTCCCTGCTCATCGTGCAGGTGTAACAGCGAGGGCAGCGAGAG	5340
Db	5413	GCTCTTTCACACAGCTTCCCTGCTCATCGTGCAGGTGTAACAGCGAGGGCAGCGAGAG	5472
OY	5341	GAGTACTTGTCTGTGTTTCCAGGAATTTGAGAGTGTCTGTGATTTCTTAACGAAAGCTATAC	5400
Db	5473	GAGTACTTGTCTGTGTTTCCAGGAATTTGAGAGTGTCTGTGATTTCTTAACGAAAGCTATAC	5532
OY	5401	CGCACAGACGATCTCAAGTGAAGTGGCTTACCTTTGGCCTTTGACCTACAGAGAACCTTAT	5460
Db	5533	CGCACAGACGATCTCAAGTGAAGTGGCTTACCTTTGGCCTTTGACCTACAGAGAACCTTAT	5592
OY	5461	CTGTGTTGACCCACTTCAACTCACTCGAAGTAATTGAGATCCAGGCAAGCTTCTCAGCA	5520

Db	5593	CTGTTTGTGACCCACTTCAACTCAGTGAATTAATGAGATCGAGGACGCTCTCAAGCA	5652
QY	5521	GGGACCCCTGCGCCGAGCGTACCTGGACATCCCGAACCCGCGCTACCTGGGCGCTGCCATT	5580
Db	5653	GGGACCCCTGCGCCGAGCGTACCTGGACATCCCGAACCCGCGCTACCTGGGCGCTGCCATT	5712
QY	5581	TCCCTAGGAGGAGATTACTATTTGCGCGTCCCTCATACAGAGATAATTAAAGGTCATTGCTGCG	5640
Db	5713	TCCCTAGGAGGAGATTACTATTTGCGCGTCCCTCATACAGAGATAATTAAAGGTCATTGCTGCG	5772
QY	5641	AAGGAAACCTCGTGAAGAGTCCGGGACTGAACACGACCGGGGCGCGTCACTCCGCG	5700
Db	5773	AAGGAAACCTCGTGAAGAGTCCGGGACTGAACACGACCGGGGCGCGTCACTCCGCG	5832
QY	5701	AGCAGCCCCCAACAGCGAGGCTCCACCGTACACAGAGCATATCACAGCGGCTGCGC	5760
Db	5833	AGCAGCCCCCAACAGCGAGGCTCCACCGTACACAGAGCATATCACAGCGGCTGCGC	5892
QY	5761	TCCAGCCCCAGGCGCGCCGAAAGGCGCCGAGCACCCCGGAGAGCGACACACCCGCG	5820
Db	5893	TCCAGCCCCAGGCGCGCCGAAAGGCGCCGAGCACCCCGGAGAGCGACACCCGCG	5952
QY	5821	TACCGCGAGGGGCGGACCGAGCTGCGGAGGAGCAAGTCTTCTGCGCGCCCCCTTGAGGCGA	5880
Db	5953	TACCGCGAGGGGCGGACCGAGCTGCGGAGGAGCAAGTCTTCTGCGCGCCCCCTTGAGGCGA	6012
QY	5881	GAGAAAGTCCCCCGGCGCGGATGCTTCAGACACCGGAGAGAGCGGTCTCCCGGAGAGCGTGT	5940
Db	6013	GAGAAAGTCCCCCGGCGCGGATGCTTCAGACACCGGAGAGAGCGGTCTCCCGGAGAGCGTGT	6072
QY	5941	GAAGACAGCAGCAAGGAGCGCGGCTGCTGCGGAGAGCGTGAAGAACCCCGCTGTCCAGAGTG	6000
Db	6073	GAAGACAGCAGCAAGGAGCGCGGCTGCTGCGGAGAGCGTGAAGAACCCCGCTGTCCAGAGTG	6132
QY	6001	AAACAAGGAAGAGGCGAGAGTGCCTCTCAAGTTTTCACGTTTAACTGTCACT	6055
Db	6133	AAACAAGGTGTGGACCAAGTCTTACAGTAAATATCTCAGCCAGAAACCAACTCTCT	6187

RESULT 12
 US-09-964-956-8
 ; Sequence 8, Application US/09964956
 ; Publication No. US20040043926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerlach, Valerie L
 ; APPLICANT: MacDougall, John R
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Miller, Isabelle
 ; APPLICANT: Stone, David
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Grose, William M
 ; APPLICANT: Alsebrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Kekuda, Rameesh
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Leach, Martin D
 ; APPLICANT: Shinkets, Richard A
 ; TITLE OF INVENTION: No. US20040043926A1 Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-124
 ; CURRENT APPLICATION NUMBER: US/09/964,956
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/235,631
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/235,633
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/235,808
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,064
 ; PRIOR FILING DATE: 2000-09-27

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PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-09-28
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/238,321
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,399
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,396
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/276,667
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/294,823
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/304,868
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 8
LENGTH: 6201
TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-956-8

Query Match 85.6%; Score 5629.8; DB 11; Length 6201;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 5929; Conservative 0; Mismatches 22; Indels 246; Gaps 4;

19 AGCTTGAAGTTCAAATATGAGCGCGGAATCTTTGATGCTGTGTGTAACCACTT 78
1 AGCTTGAAGTTCAAATATGAGCGCGGAATCTTTGATGCTGTGTGTAACCACTT 60
79 GCGAGCGGGCCCTCCAGGCGGATCTGTCTCCAGGGGAAACCACTTATGACTCA 138
61 GCGAGCGGGCCCTCCAGGCGGATCTGTCTCCAGGGGAAACCACTTATGACTCA 120
139 CAGCAGATGTCTCTCTTTCCGAGAAAGGATATAGATGCCCTCTTGTCTTTGAA 198
121 CAGCAGATGTCTCTCTTTCCGAGAAAGGATATAGATGCCCTCTTGTCTTTGAA 180
199 GAATGAGTCAAGCTCTGCTGATGAAGATTAAAGCAGTGAACCTTTGTCGGAAGTAT 258
181 GAATGAGTCAAGCTCTGCTGATGAAGATTAAAGCAGTGAACCTTTGTCGGAAGTAT 240
259 TCCGACACATAGCTAGTTAGAGAGCTCCAGCTTCGCGAAAGACTTCGAAGTCAG 318
241 TCCGACACATAGCTAGTTAGAGAGCTCCAGCTTCGCGAAAGACTTCGAAGTCAG 300
319 AGCTTGAAGTTCAGTCACTTTGCTGAAGTCAAGTGTGTAAGAGAAAGCAACCGG 378
301 AGCTTGAAGTTCAGTCACTTTGCTGAAGTCAAGTGTGTAAGAGAAAGCAACCGG 360
379 GACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATTTGGCCCAAGAGAGTTTCA 438
361 GACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATTTGGCCCAAGAGAGTTTCA 420
439 TTTTGAAGAAAGGGAACATATTATCTCGAAGCAAGCCCGTGAATCCCAATTA 498
421 TTTTGAAGAAAGGGAACATATTATCTCGAAGCAAGCCCGTGAATCCCAATTA 480
499 CAGTATGCTTTGAGAGCAAAATCACTTTATCTGATGAGGAATATCAGCTGAGG 558
481 CAGTATGCTTTGAGAGCAAAATCACTTTATCTGATGAGGAATATCAGCTGAGG 540
559 GACTTCTGTCACTTTGATATGATATGAGAGCAAGTATGATGATGATGATGATGAT 618
541 GACTTCTGTCACTTTGATATGATATGAGAGCAAGTATGATGATGATGATGATGAT 600
619 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGGTTTCATGATGGATGATGATGATGAT 678

601 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGGTTTCATGATGGATGATGATGATGATGAT 660
679 GACATCAAGCTGAGAAACATTTCTGTGACCCGACAGGACATATCAAGTGTGATTTT 738
661 GACATCAAGCTGAGAAACATTTCTGTGACCCGACAGGACATATCAAGTGTGATTTT 720
739 GATCTGCGCGGAAATGAATCAACAGATGTGATGATGATGATGATGATGATGATGATGAT 798
721 GATCTGCGCGGAAATGAATCAACAGATGTGATGATGATGATGATGATGATGATGATGATGAT 777
799 CCAGATTCATGAGCTCTGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 858
778 CCAGATTCATGAGCTCTGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 837
859 GGCCTGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 918
838 GGCCTGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
919 TCCCTCTGAGAGGAACTCTGCGAGAACCTTCAATTAATGATGATGATGATGATGATGATGAT 978
898 TCCCTCTGAGAGGAACTCTGCGAGAACCTTCAATTAATGATGATGATGATGATGATGATGAT 957
979 TTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1038
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1039 TTGTTGCGGCGCAAGAAAGAGACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1098
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1159 TCTGAGATGACCTCTCAATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1218
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1198 CCGTGCAGCTGAGCCCTCAGGCTTCTGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1257
1279 TACAGAGGCACTGGGGAATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1338
1258 TACAGAGGCACTGGGGAATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
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1318 CCGTGCAGCTGAGCTCTCAATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1377
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1459 GAGTGAAGCTGTGTTAGTGAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1518
1438 GAGTGAAGCTGTGTTAGTGAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1497
1519 TCCCTCTGAGAGGAACTCTGCTACATCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1578
1498 TCCCTCTGAGAGGAACTCTGCTACATCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1557
1579 TTGAGCAAGCAAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1638
1558 TTGAGCAAGCAAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1617
1639 GATATCAAGAGCAAGAGCCGGAAGCTTCAAGAAATCAAGAGAGAGAGAGAGAGAGAGAGAG 1698
1618 GATATCAAGAGCAAGAGCCGGAAGCTTCAAGAAATCAAGAGAGAGAGAGAGAGAGAGAGAG 1677
1699 GTGGAAGAAATGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1758

Db 1678 GTGGAAGAAATGAGTTGATGAAATCAGTTGGAAAGGATCTTGTCTCAGCAAGAAGA 1737
QY 1759 CGGAGTGAATCTCTACGAATCTGAGCTGAGAGAGTCTCGGCTTGCTGCTGAGAAATTCAG 1818
Db 1738 CGGAGGATCTCTACGAATCTGAGCTGAGAGAGTCTCGGCTTGCTGCTGAGAAATTCAG 1797
QY 1819 CGGAAAGCAGCAAGATGTGAGCTAAACTGTTGAAGGCTTAAGGATCAAGGAAAGGCTGAA 1878
Db 1798 CGGAAAGCAGCAAGATGTGAGCTAAACTGTTGAAGGCTTAAGGATCAAGGAAAGGCTGAA 1857
QY 1879 GTGGAGAAATATGCGAACTGAGAAAGATCAATGCTGAGCAGCAGCTCAAAATTCAGAG 1938
Db 1858 GTGGAGAAATATGCGAACTGAGAGAGATCAATGCTGAGCAGCAGCTCAAAATTCAGAG 1917
QY 1939 CTCCAGAGAAACTGAGAAAGGCT----- 1962
Db 1918 CTCCAGAGAAACTGAGAAAGGCTGTAAAGCCAGCAGCAGGCTGCTGAG 1977
QY 1963 -----GCAAAAGAGCGAGCGAGAGGAGCTGAGAAAGCTGAGAAAGCCGAGAG 2010
Db 1978 AATATCCGCAAGCAGCAAGAGAGCGAGCGAGAGGAGCTGAGAAAGCTGAGAAAGCCGAGAG 2037
QY 2011 GATTTCTTGAAGGATCAGAAAGAAAGCTGTGGAAGCTGAGAAAGCCGCAATTCCTG 2070
Db 2038 GATTTCTTGAAGGATCAGAAAGAAAGCTGTGGAAGCTGAGAAAGCCGCAATTCCTG 2097
QY 2071 GGAACAAGGTAAAGACTTAAGACCTAAGACCGTAAAGAAACAGACTGAAAGATGAC 2130
Db 2098 GGAACAAGGTAAAGACTTAAGACCGTAAAGACCGTAAAGAAACAGACTGAAAGATGAC 2157
QY 2131 ATCCAGACAAAATCCCAAGATCCAGAGATGAGCTGATAAATTTGAGCTCGAAGAG 2190
Db 2158 ATCCAGACAAAATCCCAAGATCCAGAGATGAGCTGATAAATTTGAGCTCGAAGAG 2217
QY 2191 AAAACATCGGAGAGCCCAAGTCTCAGCCAGCACCTAAGAAAGTGCCTGAAACGAAAGAG 2250
Db 2218 AAAACATCGGAGAGCCCAAGTCTCAGCCAGCACCTAAGAAAGTGCCTGAAACGAAAGAG 2277
QY 2251 CAGCACTATGAGGAAAGATTAAGTGTGACAAATCAGATTAAGAAACCTGAGCTGAC 2310
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QY 2311 AAGAGACACTGAGAGACATGATGACAGACACAGAGAGAGGCCATGAGAAAGGCAAA 2370
Db 2338 AAGAGACACTGAGAGACATGATGACAGACACAGAGAGAGGCCATGAGAAAGGCAAA 2397
QY 2371 ATTCTCAGGAAACAGAGGCGATGATCAATGCTATGATTCCAAGATCAGATCCTTGAA 2430
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QY 2431 CAGAGGATGTGGAACCTGTCTAAGCCATTAACCTTGACAAATTAAGCAGCTTTTAAAC 2490
Db 2458 CAGAGGATGTGGAACCTGTCTAAGCCATTAACCTTGACAAATTAAGCAGCTTTTAAAC 2517
QY 2491 CAAAGGAACATGAAAGGCCCAAGAAAGATGATTTCTGAACTCAGGCAACAGAAATTTTAC 2550
Db 2518 CAAAGGAACATGAAAGGCCCAAGAAAGATGATTTCTGAACTCAGGCAACAGAAATTTTAC 2577
QY 2551 CTGAGACACAGAGCTGGAAAGTTGAGGCCCAAGAACGAAAACTGAGAGAGCAGCTGAG 2610
Db 2578 CTGAGACACAGAGCTGGAAAGTTGAGGCCCAAGAACGAAAACTGAGAGAGCAGCTGAG 2637
QY 2611 AAGATCAGCCACCAAGACCAAGTGCAGGAATCGGCTGCTGGAAGCTGAGACCAAGATTG 2670
Db 2638 AAGATCAGCCACCAAGACCAAGTGCAGGAATCGGCTGCTGGAAGCTGAGACCAAGATTG 2697
QY 2671 CGGAGAGTCAATCTAAGACACAGAGACGAAACTGAGCTCAGGCGCAGCTCAGAG 2730
Db 2698 CGGAGAGTCAATCTAAGACACAGAGAGCAAACTGAGCTCAGGCGCAGCTCAGAG 2757
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Db 2758 CTACAGCTTCTCCTGACAGAGCGCAGATCAAGTTGACAGCCTGACAGGCTGACAGGCG 2817

QY 2791 GCCCTGAGAGCCAGCTTCCAGCGCAAGACAGAGCTGGAAGAGACCAAGCAGAGAGCT 2850
Db 2818 GCCCTGAGAGCCAGCTTCCAGCGCGAAGACAGAGCTGGAAGAGACCAAGCAGAGAGCT 2877
QY 2851 GAAAGAGAGATCAGGCACTCAGGCACTAGAGATGAAATCAGCGCAAAATTTGATGCT 2910
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QY 2911 CTTGTAACAGCTGTACTGTAAATCAAGACCTGAGAGCAGCTTAAACAGCTGACCGAG 2970
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QY 3031 GGCAGCAAGCAGAGATTTGACAACTGGAAGTGAAGTGAACCATCTCGCGGAGATC 3090
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QY 3151 TGCACCATGCTGAGAGAAACAGGTCAATGATTTGAGAGGCCCTTAAACGATAGAGCTGAGAA 3210
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QY 3211 AAAGAGCGGAGTGGAGAGGCTGAGAGAGCGTCTGAGGATGAGAAATCCAGTTTGA 3270
Db 3238 AAAGAGCGGAGTGGAGAGGCTGAGAGAGCGTCTGAGGATGAGAAATCCAGTTTGA 3297
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QY 3331 GATCAGCGGATCAACGAGTCTCCGAGGTGATGAGAGCTGAGAGCAAGAGCT 3390
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QY 3391 GAGATTTCTGCTGTCAGACAGAGCTCTCAAGAGCAGAAAGCTGAAAGCGAGAGCTCTCT 3450
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QY 3691 GAAAAATTCAGGTTTCTATTTCTATGAAAGGGAAGGAAAGGAGCAATTTCTCAA 3750
Db 3718 GAAAAATTCAGGTTTCTATTTCTATGAAAGGGAAGGAAAGGAGCAATTTCTCAA 3777
QY 3751 CAAACCAAACTCATTTGATTTCTGCAAGCCAAATGAGCAACCTGCTTAAAGAAAAAG 3810
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Db 3836 -----AGTGCCCTCTCAGATAC 3852

3871 AATGAGCTGAAGCTGGCCCTGGAGAGAGAAAGCTCGCTGTGTCAGAGCTAAGAGAGCC 3930
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3931 CTTGAGAGAGCCGCACTGAGCTCCGGTCCGCCGGAGAGAGCTCCCAACCGCAAGCA 3990
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3991 ACGGAGCCAGCCAGCCATCCAGCGAGCCAGCGAGAGAGAGATCCGATGTCCGCC 4050
3973 ACGGAGCCAGCCAGCCATCCAGCGAGCCAGCGAGAGAGAGATCCGATGTCCGCC 4032
4051 ATGTGCGGTTCGCAAGAGAGCCAGCGAGCCAGCGAGAGAGATCCGATGTCCGCC 4110
4033 ATGTGCGGTTCGCAAGAGAGCCAGCGAGCCAGCGAGAGAGATCCGATGTCCGCC 4092
4111 CCGAGAGAGAGCTTCAACTCCAGAGAGATTTAGTCCGCTTTAAGAGAGCATGCA 4170
4093 CCGAGAGAGAGCTTCAACTCCAGAGAGATTTAGTCCGCTTTAAGAGAGCATGCA 4152
4171 CACAAATATTCTTCACCGGATTCAGAGCTGAGAGATGAGAGCCAGAAATGTCTGTG 4230
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4231 TGTCTGATTAACCTGCACTTTGAGAGCCAGGATCCAAATGTCTGAAATGTCTGTG 4290
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4291 TGTCAACCCAGAGCTTCAAGCTGCTTGCAGAGCCAGCTGCGGCTGTGCTGAAATG 4350
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4633 GCAAGATGCCATACATCTAGAGATGGAATCTCACCCGACACACCTGTGCCCCGG 4692
4654 ----- 4653
4693 AGAACCCTTACTTGTAGCTCCAGGCTTCTGACAAACAGCGCTGAGTCAACGCTT 4752
4654 ----- 4653
4753 GAAATGATGTGCGAGGTGGAGAGTTTCTAGAGAGAGAGAGAGAGAGAGAGAGAG 4812
4681 CTTGAGAGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4740
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4741 CCGTTGAG 4800
4873 CCGTTGAG 4932
4801 TTGAG 4860

4933 TTGAG 4992
4861 AAG 4920
4993 AAG 5052
4921 GTGAG 4980
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4981 CCAAG 5040
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5041 GAG 5100
5173 GAG 5232
5101 CAG 5160
5233 CAG 5292
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5281 GCGTCTTCAAG 5340
5413 GCGTCTTCAAG 5472
5341 GAGTCTTCAAG 5400
5473 GAGTCTTCAAG 5532
5401 CAG 5460
5533 CAG 5592
5461 CAG 5520
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5521 GAG 5580
5653 GAG 5712
5581 TCCTCAG 5640
5713 TCCTCAG 5772
5641 AAG 5700
5773 AAG 5832
5701 AAG 5760
5833 AAG 5892
5761 TCCAG 5820
5893 TCCAG 5952
5821 TCCAG 5880
5953 TCCAG 6012
5881 GAG 5940

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Db      6013 GAGAGTCCCCCGCGGATGTCAGCACCGGAGAGCGGTCCCCCGGAGGCTGT 6072
Qy      5941 GAGAGCAGCAGCGGCGCGCTGCTGCGCGGAGCGGTGAGACCCCGCTGTCCAGGTG 6000
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Qy      6001 AACAGGAGAGAGGCGCA 6017
Db      6133 AACAGGTGAGGACGCA 6149

RESULT 13
US-10-262-511-13
; Sequence 13, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojie (Sasha)
; APPLICANT: Paturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Caterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkels, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Cureseqblast version 0.1
; SEQ ID NO 13
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; LENGTH: 6201
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(6198)
US-10-262-511-13

Query Match      85.6%; Score 5629.8; DB 17; Length 6201;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 5929; Conservative 0; Mismatches 22; Indels 246; Gaps 4;

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Qy      79  GCCAGCCGGGCTCCAGGCTGAATCTGTTCTCCAGGGAAACCACTTTATGACTCA 138
Db      61  GCCAGCCGGGCTCCAGGCTGAATCTGTTCTCCAGGGAAACCACTTTATGACTCA 120
Qy      139  CAGCAGATGTCCTCTTTCCGAGAGGATATTAGATGCCCTTGTCTTTGAA 198
Db      121  CAGCAGATGTCCTCTTTCCGAGAGGATATTAGATGCCCTTGTCTTTGAA 180
Qy      199  GAATGACATGACCGCTGCTGATGAGATTAGACCGGACCACTTTGCGGAGTAT 258
Db      181  GAATGACATGACCGCTGCTGATGAGATTAGACCGGACCACTTTGCGGAGTAT 240
Qy      259  TCCGACACCATAGCTGAGTTACAGAGAGCTCCAGCTTCGCAAGAGACTTGAATCAGA 318
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Qy      319  AGCTTTGAGTTGTTGGTCACTTTGCTGAAGTCAAGTGTGAAGAGAAACGCGG 378
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Qy      439  TTTTGTGAGAAAGACCGGACATATTATCTGAAACCAAGCCCGTGATCCCCAATTA 498
Db      421  TTTTGTGAGAAAGACCGGACATATTATCTGAAACCAAGCCCGTGATCCCCAATTA 480
Qy      499  CAGTATGCTTTCAAGCAAAATACCTTATATGATGAGAAATACAGCTGAGAGG 558
Db      481  CAGTATGCTTTCAAGCAAAATACCTTATATGATGAGAAATACAGCTGAGAGG 540
Qy      559  GACTTGCTGCTCACTTTGAATAGATAGAGACCAAGTTAGTAAACCTGATCAGTTT 618
Db      541  GACTTGCTGCTCACTTTGAATAGATAGAGACCAAGTTAGTAAACCTGATCAGTTT 600
Qy      619  TACCTAGCTAGCTGATTTTGGCTGTTCAAGCGTTATCTGATGAGATACGTGATCGA 678
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Qy      679  GACATCAAGCCTGAGAACTTCGTTGACCGGACAGACACATCAAGCTGAGGATTTT 738
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Qy      799  CCAGATTACATGCTCTCTGAAGTCTGATGATGAACCGGGATGAGAAAGGACCTTAC 858
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Qy      859  GGCTTGACTGTGACTGAGTGTGAGTGGGAGGTATGCTTATGATGATGATTTATGGAGA 918
Db      838  GGCTTGACTGTGACTGAGTGTGAGTGGGAGGTATGCTTATGATGATGATTTATGGAGA 897
Qy      919  TCCCTTTCAGAGGGAACCTCTGCGAGAACCTTCAATTAATTAATTTCCAGCGG 978
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Db 898 TCCCTTCGAGAGGGAACTCTGCCAGAACTTCAATAAGTAATGATTTCCAGCG 957
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Qy 1039 TTGTGTGCGGCGAGAAAGAGACTGAGTTGAAGTCTTTGCTCCATCCCTTTTC 1098
Db 1018 TTGTGTGCGGCGAGAAAGAGACTGAGTTGAAGTCTTTGCTCCATCCCTTTTC 1077
Qy 1099 TCTAAATTTGACTGAACAACATTCGTACTCTCCCTCTGTTCCCACTCCAG 1158
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Qy 1159 TCTGACGATGACACTTCCAAATTTTGTATGAACAGAGAAATTCGTGGTTTCACTCT 1218
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Qy 1279 TACAGCAAGGCACTGGGGATTTCTTGATGATCTGATCTGTGTGTCGGGTCGACTCC 1338
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Db 1378 TCTCAGAGCAAGTGTCAAGATGAGAGCAAGAAATGAACCCGGTTACATCGGAAGTCA 1437
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Qy 1639 GATATCAGAGAGAGAGCCGGAAGCTCAAGAAATCAAGAGAGAGTACAGGCTCAA 1698
Db 1618 GATATCAGAGAGAGAGCCGGAAGCTCAAGAAATCAAGAGAGAGTACAGGCTCAA 1677
Qy 1699 GTGGAAGAAATGAGGTTGATGATGAATCAGTTGGAAGAGATCTTGTCTCAGCAAGAGA 1758
Db 1678 GTGGAAGAAATGAGGTTGATGATGAATCAGTTGGAAGAGATCTTGTCTCAGCAAGAGA 1737
Qy 1759 CGGAGTATCTTCAAGAAATCTGAGCTGAGAGAGTCTTGGCTTGTCTGTAAGAAATCAAG 1818
Db 1738 CGGAGTATCTTCAAGAAATCTGAGCTGAGAGAGTCTTGGCTTGTCTGTAAGAAATCAAG 1797
Qy 1819 CGGAAGCGAGAGATGTGACATTAACCTGTTGAAGCTTAAGATCAAGGAGAGCTGAAG 1878
Db 1798 CGGAAGCGAGAGATGTGACATTAACCTGTTGAAGCTTAAGATCAAGGAGAGCTGAAG 1857
Qy 1879 GTGGAGAAATATCGAAATCTGAGAGAGATCAATGCTGAGAGAGAGCTCAAAATTCAGAG 1938
Db 1858 GTGGAGAAATATCGAAATCTGAGAGAGATCAATGCTGAGAGAGAGCTCAAAATTCAGAG 1917
Qy 1939 CTCCAAGAAATCTGAGAGAGCT----- 1962
Db 1918 CTCCAAGAAATCTGAGAGAGCTGTAAGAGCAAGAGCTCAAGAGCTGTCAG 1977
Qy 1963 -----GCAAGAGAGAGCTGAGAGAGAGCTGAGAGAGCTGCAAGCCGAGAG 2010

Db 1978 AATATCCGACGAGCAAAAGAGCGAGCCGAGAGAGCTGTAGAAAGCTGCAGAACGAGAG 2037
Qy 2011 GATTTCTTGAAGGATTCAGAAAGAGCTGTGGAAGCTGAGGAACGCCGCTTCTTCG 2070
Db 2038 GATTTCTTGAAGGATTCAGAAAGAGCTGTGGAAGCTGAGGAACGCCGCTTCTTCG 2097
Qy 2071 GAGAACAGGTAAAGACTAGAGACCATGAGCGTGAAGAAACAGACTGAAGATGAC 2130
Db 2098 GAGAACAGGTAAAGACTAGAGACCATGAGCGTGAAGAAACAGACTGAAGATGAC 2157
Qy 2131 ATCCAGACAAATCCCAAGATTCAGAGAGATGCTGATTAATTTGTGAGCTCGAAGAG 2190
Db 2158 ATCCAGACAAATCCCAAGATTCAGAGAGATGCTGATTAATTTGTGAGCTCGAAGAG 2217
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Db 2338 AAGGAGACACTGAGAGACATGATGACAGACACAGAGAGAGGCCATGAGAAAGGCAAA 2397
Qy 2371 ATTCTCAGGAAACAGAGCGATGATCAATGCTATGATTTCCAGATTCATCCTCGAA 2430
Db 2398 ATTCTCAGGAAACAGAGCGATGATCAATGCTATGATTTCCAGATTCATCCTCGAA 2457
Qy 2431 CAGAGATTGTGGAACGTCTGAAGCCATTAACCTTGAGCAAAATGAGCTTTTAC 2490
Db 2458 CAGAGATTGTGGAACGTCTGAAGCCATTAACCTTGAGCAAAATGAGCTTTTAC 2517
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Db 2518 CAAAGGAATGAGAGCCCAAGAGAGATGATTTGAACTCAGGCAACAGAAATTTTAC 2577
Qy 2551 CTGAGACACAGGCTGGGAAGTTGAGAGCCAGAACCGAAATCTGAGAGAGAGCTGAG 2610
Db 2578 CTGAGACACAGGCTGGGAAGTTGAGAGCCAGAACCGAAATCTGAGAGAGAGCTGAG 2637
Qy 2611 AAGATGAGCCACCAAGACCAAGTGAAGAAATGCGCTGAGAACTGAGACCAAGATTG 2670
Db 2638 AAGATGAGCCACCAAGACCAAGTGAAGAAATGCGCTGAGAACTGAGACCAAGATTG 2697
Qy 2671 CCGGAGGTCAGTCTAGAGACAGAGAGCAGAAATGAGCTCAAGCGCAGCTCACAGAG 2730
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Db 2758 CTACAGCTTCTCCCTGAGAGAGCGGAGTCAAGTTGACAGCCCTGAGCTCAAGCGCG 2817
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Db 2818 GCCCTGGAAGGCAAGCTTGGCCAGCGGAGAGACAGAGCTGGAAGAGACCAAGAGAGCT 2877
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Db 2878 GAAAGAGATTCAGGCACTCAGGCACTAAGATGAATTCAGCGCAAAATTTGTATGCT 2937
Qy 2911 CTTTCTGACGCTGTACTGTAAATCAAGACTGAGAGAGCTTAACAGCTGACCGAG 2970
Db 2938 CTTTCTGACGCTGTACTGTAAATCAAGACTGAGAGAGCTTAACAGCTGACCGAG 2997
Qy 2971 GACAAAGCTGAAGCTCAACCAAACTTCACTTGTCCAAACACTGATGAGCTTCT 3030
Db 2998 GACAAAGCTGAAGCTCAACCAAACTTCACTTGTCCAAACACTGATGAGCTTCT 3057
Qy 3031 GCGGCAACGAGAGATTGTACACTGCAAGTGAAGTGAACATTCGCGCGGAGATC 3090
Db 3058 GCGGCAACGAGAGATTGTACACTGCAAGTGAAGTGAACATTCGCGCGGAGATC 3117

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Db	3118	ACGGAAAGAGAGATGACGCTTACAGCCAGAAAGCAAGATGAGGCTCTGAAGCAACG	3177	Db	4153	CACAAATATCTCACCAGATTCAACGTAAGACTGAA CATGCGAGCCAAAGTGTGCTGTG	4212
QY	3151	TGCACATGCTGAGAGAAACAGTGCATGATTTGGAGGCCCTTAAACGATGAGTGTGAA	3210	QY	4231	TGCTGTGATTAACGCTGCACCTTTGAGCGCAGGGAATCCAAATGCTCTGAAATGTCAAGTGTG	4290
Db	3178	TGCACATGCTGAGAGAAACAGTGCATGATTTGGAGGCCCTTAAACGATGAGTGTGAA	3237	Db	4213	TGCTGTGATTAACGCTGCACCTTTGAGCGCAGGGAATCCAAATGCTCTGAAATGTCAAGTGTG	4272
QY	3211	AAAGAGGGGAGATGGGAGGCTCTGAGAGAGCTCTGGGTGATGAGAAATCCAGTTTGA	3270	QY	4291	TGTCAACCCCAAGTGTCCAAGTCTTGGCAGCACTGCGGCTTCCGCTGTAATATATG	4350
Db	3238	AAAGAGGGGAGATGGGAGGCTCTGAGAGAGCTCTGGGTGATGAGAAATCCAGTTTGA	3297	Db	4273	TGTCAACCCCAAGTGTCCAAGTCTTGGCAGCACTGCGGCTTCCGCTGTAATATG	4332
QY	3271	TGTGCGGTTGAGAGCTGACAGAAATGCTGACACCGAGAAACAGAGCAGGGGAGAGCC	3330	QY	4351	ACACATTTCAACGAGGCTTCTGCGGTGACAAATGAACTCCCAAGTCTTCAGCAAG	4410
Db	3298	TGTGCGGTTGAGAGCTGACAGAAATGCTGACACCGAGAAACAGAGCAGGGGAGAGCC	3357	Db	4333	ACACATTTCAACGAGGCTTCTGCGGTGACAAATGAACTCCCAAGTCTTCAGCAAG	4392
QY	3331	GATCAGGGGATCACCCAGTCTCCCAAGTGTGTGAGCTGGCAGTGAAGCACAAGGCT	3390	QY	4411	GAGCCACAGAGCTTGCACCTGGAGGGTGAATGAAGGTGCCAGGAATTAACAAAGA	4470
Db	3358	GATCAGGGGATCACCCAGTCTCCCAAGTGTGTGAGCTGGCAGTGAAGCACAAGGCT	3417	Db	4393	GAGCCACAGAGCTTGCACCTGGAGGGTGAATGAAGGTGCCAGGAATTAACAAAGA	4452
QY	3391	GAGATTCGTGCTGACAGAGGCTCTCAAGAGCAAGAGCTGAAGGCCGAGAGCTCTCT	3450	QY	4471	GGACAGCAAGGCTGGACAGGAAGTACATTTGCTGAGGAGATCAAAAGTCTCATTTAT	4530
Db	3418	GAGATTCGTGCTGACAGAGGCTCTCAAGAGCAAGAGCTGAAGGCCGAGAGCTCTCT	3477	Db	4453	GGACAGCAAGGCTGGACAGGAAGTACATTTGCTGAGGAGATCAAAAGTCTCATTTAT	4512
QY	3451	GACAACTCAATGACCTGAGAGAAAGACATGCTATGCTTGAATGAATGCGGAGCTTA	3510	QY	4531	GACAAATGAAGCCAGAGAGCTGGAACAGAGGCCGTGGAAAGATTTGAGCTGTGCTTCC	4590
Db	3478	GACAACTCAATGACCTGAGAGAAAGACATGCTATGCTTGAATGAATGCGGAGCTTA	3537	Db	4513	GACAAATGAAGCCAGAGAGCTGGAACAGAGGCCGTGGAAAGATTTGAGCTGTGCTTCC	4572
QY	3511	CAGCAAGAGCTGAGACCTGAACAGAGAGCTCAACAGAGGCTCTTGAAGAGCAAGCCAA	3570	QY	4591	GACGGGATGTATCTATCTCATGCTGCGGTGCTTCCGAACTCCGAAATTAACGACAA	4650
Db	3538	CAGCAAGAGCTGAGACCTGAACAGAGAGCTCAACAGAGGCTCTTGAAGAGCAAGCCAA	3597	Db	4573	GACGGGATGTATCTATCTCATGCTGCGGTGCTTCCGAACTCCGAAATTAACGACAA	4632
QY	3571	TTACAGCAGACAGATGAGACCTGACGAAAAATCACATTTCCGTCTGCTCAAGACCTGCA	3630	QY	4651	GCA-----	4653
Db	3598	TTACAGCAGACAGATGAGACCTGACGAAAAATCACATTTCCGTCTGCTCAAGACCTGCA	3657	Db	4633	GCAATGTCCATACATAGTAGATGAATCTCACCCGACACACACTGCTGCGCGG	4692
QY	3631	GAACTCTAGATCGGCTGATCTTAAGAGACAGAAAGATGACTTGGAGTATGACTG	3690	QY	4654	-----	4653
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QY	3691	GAAAGATTCAGAGTTCTTAATCTCATGAAAGGTGAAATGAAAGGCACTATTTCTCA	3750	QY	4654	-----	4653
Db	3718	GAAAGATTCAGAGTTCTTAATCTCATGAAAGGTGAAATGAAAGGCACTATTTCTCA	3777	Db	4633	GCAATGTCCATACATAGTAGATGAATCTCACCCGACACACACTGCTGCGCGG	4692
QY	3751	CAAACCAAACTGATGATTTTCTGCAAGCCAAATGAGCAACCTGCTTAAAGAAAAAG	3810	QY	4681	CTTGGAAATCTCCCTGCTGAAACTGGAAGGTGATGACCTGTACATGAATGACGCTG	4740
Db	3778	CAAACCAAACTGATGATTTTCTGCAAGCCAAATGAGCAACCTGCTTAAAGAAAAAG	3835	Db	4681	CTTGGAAATCTCCCTGCTGAAACTGGAAGGTGATGACCTGTACATGAATGACGCTG	4740
QY	3811	GGTTTATTTAGTCAGCGAAAGAGACCTGCTTTAACCAACAGGTTCTCTGCAGTAC	3870	QY	4741	CCCTTCAGTGAACAGGTGTGTGTGTGTGGGACCGAGGAAGGGCTCTACGCTGGAATGTC	4800
Db	3836	-----	3852	Db	4741	CCCTTCAGTGAACAGGTGTGTGTGTGTGGGACCGAGGAAGGGCTCTACGCTGGAATGTC	4800
QY	3871	AATGAGCTGAAGCTGGCCCTGAGAGAGAAAGCTCCGTGTGACAGACTGAGAGAAC	3930	QY	4801	TTGAAAACTCCCTTAACCAATGTCCTCCAGAAATGAGCACTTCTCCAAATTTATATATC	4860
Db	3853	AATGAGCTGAAGCTGGCCCTGAGAGAGAAAGCTCCGTGTGACAGACTGAGAGAAC	3912	Db	4801	TTGAAAACTCCCTTAACCAATGTCCTCCAGAAATGAGCACTTCTCCAAATTTATATATC	4860
QY	3931	CTTCAAGAAAGCCGATGAGCTCCGATCCGCGGAGAGAGCTGCCACCGCAAAACA	3990	QY	4933	TTGAAAACTCCCTTAACCAATGTCCTCCAGAAATGAGCACTTCTCCAAATTTATATATC	4992
Db	3913	CTTCAAGAAAGCCGATGAGCTCCGATCCGCGGAGAGAGCTGCCACCGCAAAACA	3972	Db	4933	TTGAAAACTCCCTTAACCAATGTCCTCCAGAAATGAGCACTTCTCCAAATTTATATATC	4992
QY	3991	ACGGACCAACCAACCACTCCACGCGCAGCCACCGGAGGAGAGAGATGCAATGTCCGC	4050	QY	4861	AAAGAACTGGAAGAGCTACATGATGAGAGAGAGAGAGGAGGCACTGTCTTGTGAC	4920
Db	3973	ACGGACCAACCAACCACTCCACGCGCAGCCACCGGAGGAGAGAGATGCAATGTCCGC	4032	Db	4861	AAAGAACTGGAAGAGCTACATGATGAGAGAGAGAGAGGAGGCACTGTCTTGTGAC	4920
QY	4051	ATCGTGGGTGCGCAGAGACCAAGCCCAAGTGCATGAGCTGTGCGGCCCGCCCATCCAGC	4110	QY	4993	AAAGAACTGGAAGAGCTACATGATGAGAGAGAGAGAGGAGGCACTGTCTTGTGAC	5052
Db	4033	ATCGTGGGTGCGCAGAGACCAAGCCCAAGTGCATGAGCTGTGCGGCCCGCCCATCCAGC	4092	Db	4993	AAAGAACTGGAAGAGCTACATGATGAGAGAGAGAGAGGAGGCACTGTCTTGTGAC	5052
QY	4111	CGCAGAAAGAGTCTTCACTTCAGAGAAATTTAGTGGCGTCTTTAAGAAACGATGAC	4170	QY	4981	CCCAACATTTTGAAGTGTCAAGGCTGCACTTGTGTGGGAGGAGCAAGATTGAAGAAC	5040
Db	4093	CGCAGAAAGAGTCTTCACTTCAGAGAAATTTAGTGGCGTCTTTAAGAAACGATGAC	4152	Db	4981	CCCAACATTTTGAAGTGTCAAGGCTGCACTTGTGTGGGAGGAGCAAGATTGAAGAAC	5040
QY	5041	GGGCTGTGATCTGTGAGCAGTCCAGGAGCAAGTGTGATTTCTCCGCTACAAAGAAAC	5100	QY	5113	CCCAACATTTTGAAGTGTCAAGGCTGCACTTGTGTGGGAGGAGCAAGATTGAAGAAC	5172
Db	5173	GGGCTGTGATCTGTGAGCAGTCCAGGAGCAAGTGTGATTTCTCCGCTACAAAGAAAC	5232	Db	5113	CCCAACATTTTGAAGTGTCAAGGCTGCACTTGTGTGGGAGGAGCAAGATTGAAGAAC	5172
QY	5101	CTCAGCAAAATACATCCGAGAAAGAGATAGAGACTTCAGAGCCCTGACGCTGTATCAC	5160	QY	5041	GGGCTGTGATCTGTGAGCAGTCCAGGAGCAAGTGTGATTTCTCCGCTACAAAGAAAC	5100

Db 5233 CTCAGAAATATGCAATCCGGAAGAGATGAGACCTCAGAGCCCTGCAGCTATACAC 5292
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Oy 5221 TACAGCTGAGGAATTTCTGATAGATGACATTTCTTGACACTCTGTGTGTTGCC 5280
Db 5353 TACAGCTGAGGAATTTCTGATAGATGACATTTCTTGACACTCTGTGTGTTGCC 5412
Oy 5281 GCCTCTTCAACAGCTTCCCTGCTCAATCTGTCAGAGTGAACAGGCGAGCGAGAG 5340
Db 5413 GCCTCTTCAACAGCTTCCCTGCTCAATCTGTCAGAGTGAACAGGCGAGCGAGAG 5472
Oy 5341 GAGTACTGCTGTGTTCACGAAATTTGAGTGTGTGATTTTACGAGAGAGCTTAC 5400
Db 5473 GAGTACTGCTGTGTTCACGAAATTTGAGTGTGTGATTTTACGAGAGAGCTTAC 5532
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Oy 5641 AAGGGAACCTCGTGAAGAGTCCGGCACTGAACACCAACCGGAGCCCGTCACTCCGCG 5700
Db 5773 AAGGGAACCTCGTGAAGAGTCCGGCACTGAACACCAACCGGAGCCCGTCACTCCGCG 5832
Oy 5701 AAGGAGCCCAACAGAGAGGCGCCACCACTGACAGAGATCAACCAAGCGCGTGGCC 5760
Db 5833 AAGGAGCCCAACAGAGAGGCGCCACCACTGACAGAGATCAACCAAGCGCGTGGCC 5892
Oy 5761 TCCAGCCCAAGCGCGCCCGGAGGCGCCAGCCACCCCGGAGAGCAACCCACCGC 5820
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Oy 5821 TACCGGAGGAGGAGGAGGCGGAGGCGGAGGAGCAAGTCTGCGGCGCCCGTGAAGCA 5880
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Oy 6001 AACAGAGAGAGGAGCA 6017
Db 6133 AACAGAGAGAGGAGCA 6149

RESULT 14
US-10-028-946-3
; Sequence 3, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fridde, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1el Human Kinases and Polynucleotides Encoding

FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-3
Query Match 81.5%; Score 5358; DB 13; Length 5877;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5634; Conservative 0; Mismatches 5; Indels 243; Gaps 3;
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Db 1 ATGTGAAGTTCAATATGAGAGCGGAAATCTTTGATGCTGTGCTGTAACCAT 60
Oy 79 GCCAGCCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCTTTATGACTCA 138
Db 61 GCCAGCCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCTTTATGACTCA 120
Oy 139 CAGCAGATGTCCTCTTTCCGAGAGGAGATTAAGATGCTGCTGTTGCTTTGAA 198
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Db 181 GAATGAGTCAAGCTGCTGATGAAGATTAAGACAGTGAAGCAATTTGTCCGAGAT 240
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Db 241 TCCGACCATATAGCTGATTAAGAGCTCCAGCTTCCGCAAGAGCTTCCAGTCA 300
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Db 301 AGCTTGTAGTGTGCTGATCTTCTGTAAGTGAAGTGAAGAGAGAGCAACCGG 360
Oy 379 GACATCTATGATGAAGATGAAGAGAGCTTTATTTGAGGAGAGAGAGGATTTCA 438
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Oy 439 TTTTGTAGAGAGAGGAGCAATATTATCTGAAGCAAGCCCGTGAATCCCAATTA 498
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Db 541 GACTTGTCTCACTTTTGAATAGATGAAGACAGATTAAGAGAGAGAGAGAGAGTT 600
Oy 619 TACCTAGCTGAGCTGATTTTGTGCTTCAAGGTTCACTGATGAGATGATGCA 678
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Oy 679 GACATCAAGCTGAGAGCAATCTCGCTGACCCGACAGAGACATCAAGCTGAGATTT 738
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Db 781 CAGATTAATGAGCTCTGATGATGCTGATGATGATGATGATGATGATGATGATGAT 840

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 QY 3811 GGTATTATTAGTGAAGAGAAAGAACCCCTTTACCAACAGAGTCCCTGCAAGTAC 3870
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 QY 3871 AATGAGCTGAGTGGCCCTGAGAGAGAGAAAGCTGCTGTGACAGATGAGAGAGCC 3930
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 QY 3931 CTTTCAAGAGACCGCATGAGCTCCGGTCCGCCGAGAGAGACTGCCCAACGCAAGCA 3990
 Db 3916 CTTTCAAGAGACCGCATGAGCTCCGGTCCGCCGAGAGAGACTGCCCAACGCAAGCA 3975
 QY 3991 AGGAGCAACCCCAACCATCCAGCCAGCCACCGGAGAGAGAGATGCGCAAGTCCGCC 4050
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 QY 4051 ATGCTGCGGTGCGCAGAGCAACGAGCCAGTGCATGAGCTGTGCGCCCGCATCCAGC 4110
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 QY 4981 CCCAATTTTGAAGCTGTCAAGGCTGCACTTGTGAGGACAGGCAAGATTGAGAAC 5040
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QY	5041	GGGCTCTGCATTTGTGGCAGCCATGCCACGAAAGTCGATTTCTTCGCTCAACAGAAAC	5100
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QY	5101	CTCAGCAAAATCTGCATCCGGAAAGAGTAAAGACCTCAGAGCCCTGACCTGATTCAC	5160
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QY	5221	TACAGGCTCGAGGAATTTCTGGATTAAGATGACATTCCTTTGAGCACTGCTGTGTGGC	5280
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QY	5281	GCCCTTTCACACAGCTTCCCTGTCTCAATCGTGGAGGTGAACAGCGAGGCGAGCGAGAG	5340
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QY	5401	CGCACAAGCAGATCTTCAAGTGAAGTCGCTTACCTTTGGCTTTGCTACAGAAACCTTAT	5460
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QY	5461	CTGTTTGTGACCCCACTTCAACTCACTCGAAGTAAATTGATTCACAGGACGCTCTGACGA	5520
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QY	5521	GGGACCCCTGCCGAGCGGTACCTTGAGATCCCGAACCCGCGCTACCTTGAGCCCTGACAT	5580
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QY	5581	TCCCTCAGAGGAGATTTACTTGGCGCTCTCATATCAGAGATTAATTAAGGGTCAATTTGCTGC	5640
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Db	5836	AG 5837	
RESULT 15			
US-10-791-666-3			
; Sequence 3, Application US/10791666			
; Publication No. US20040209297A1			
; GENERAL INFORMATION:			
APPLICANT: Yu, Xuanchuan			
APPLICANT: Miranda, Maricar			
TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same			
FILE REFERENCE: LEX-0289-USA			
CURRENT APPLICATION NUMBER: US/10/791,666			
CURRENT FILING DATE: 2004-03-02			
PRIOR APPLICATION NUMBER: US/10/028,946			
PRIOR FILING DATE: 2001-12-20			
PRIOR APPLICATION NUMBER: US 60/258,315			
PRIOR FILING DATE: 2000-12-27			
NUMBER OF SEQ ID NOS: 4			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 3			
LENGTH: 3877			
TYPE: DNA			
ORGANISM: homo sapiens			
US-10-791-666-3			

Query Match	81.5%;	Score 5358;	DB 18;	Length 5877;
Best Local Similarity	95.8%;	Pred. No. 0;		
Matches 5634;	Conservative	0;	Mismatches 5;	Indels 243;
				Gaps 3

QY	15	ATGTTGAAGTTCAAATATGAGAGCGGGAATCCTTTGATGCTGTCGTGTGAACCCATT	78
Db	1	ATGTTGAAGTTCAAATATGAGAGCGGGAATCCTTTGATGCTGTCGTGTGAACCCATT	60
QY	79	GCAGCGCGGAGCCCTCCAGGCTGAAATCTGTTCTTCAGGGGAAACCACTCTTATGACTCA	138
Db	61	GCCAGCGGAGCCCTCCAGGCTGAAATCTGTTCTTCAGGGGAAACCACTCTTATGACTCA	120
QY	139	CAGCAGATGTCCTTCCTTTCCGAGAGGGGATATTAAGTGCCTCTTGTCTCTTTGAA	198
Db	121	CAGCAGATGTCCTTCCTTTCCGAGAGGGGATATTAAGTGCCTCTTGTCTCTTTGAA	180
QY	199	GAATGACGTACAGCGCTGCTGATGAAATTAAGCACTGTAGCAACTTTGTCCGAGATAT	258
Db	181	GAATGACGTACAGCGCTGCTGATGAAATTAAGCACTGTAGCAACTTTGTCCGAGATAT	240
QY	259	TCCGACACCATATAGCTAGTTTACAGAGAGCTCCAGCCTTCGGCAAAAGGACTTCGAAATCAG	318
Db	241	TCCGACACCATATAGCTAGTTTACAGAGAGCTCCAGCCTTCGGCAAAAGGACTTCGAAATCAG	300
QY	319	AGTCTTGTATGTTTGTGTGTCACTTTGTGAATGTGACGTGTAAAGAGAAACACCGG	378
Db	301	AGTCTTGTATGTTTGTGTGTCACTTTGTGAATGTGACGTGTAAAGAGAAACACCGG	360
QY	379	GACATCTATGCTATGAAAGTATGATGAAGAAAGGCTTTTATGGCCAGAGACAGTTTGA	438
Db	361	GACATCTATGCTATGAAAGTATGATGAAGAAAGGCTTTTATGGCCAGAGACAGTTTGA	420
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Db	421	TTTTTTGAGAAAGACCGGAACATATATCTCGAAGCACAAAGCCGTGATCCCCCAATTA	480
QY	499	CAGTATGCTTTCAAGACAAAATCACTTTATCTGATGGAAGAAATATACGCTGAGGG	558
Db	481	CAGTATGCTTTCAAGACAAAATCACTTTATCTGATGGAAGAAATATACGCTGAGGG	540
QY	559	GACTTGCTGTCACTTTTGATATGATATGAGACACAGTTAGATGAAGAACTGTATACGTTT	618
Db	541	GACTTGCTGTCACTTTTGATATGATATGAGACACAGTTAGATGAAGAACTGTATACGTTT	600
QY	619	TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTTCATCTGATGAGATACGTGATCGA	678
Db	601	TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTTCATCTGATGAGATACGTGATCGA	660
QY	679	GACATCAAGCCGTGAAGACATTCGTGTACACGACACAGACACATCAAGCTGTGATTTT	738
Db	661	GACATCAAGCCGTGAAGACATTCGTGTACACGACACAGACACATCAAGCTGTGATTTT	720
QY	739	GGATCTGCGCGGAAAATGAATTCAAACAAGATGTGAAATGCCMAATCCCGATTTGGGACC	798
Db	721	GGATCTGCGCGGAAAATGAATTCAAACAAGATGTGAAATGCCMAATCCCGATTTGGGACC	780
QY	799	CCAAGTTATCATGCTCTCTGAAGTGTGTACTGTATGAAACGGGGATGGAAGGCACTTAC	858
Db	781	CCAAGTTATCATGCTCTCTGAAGTGTGTACTGTATGAAACGGGGATGGAAGGCACTTAC	840
QY	859	GAGCTGAGACTGTGACTGTGTCTAGTGGGCGTGAATTTGCTATGAGATATTTATGGGAGA	918
Db	841	GAGCTGAGACTGTGACTGTGTCTAGTGGGCGTGAATTTGCTATGAGATATTTATGGGAGA	900
QY	919	TCCCTCTTTCGACAGGGGAACCTCTGACGAACCTTCAATTAACATTAATGATTTCCAGCG	978
Db	901	TCCCTCTTTCGACAGGGGAACCTCTGACGAACCTTCAATTAACATTAATGATTTCCAGCG	960
QY	979	TTTTTGAATTTCCAGATGACCCCAAGGTGAGAGCTTCTTGTGATCTGATTTCAAGC	1038
Db	961	TTTTTGAATTTCCAGATGACCCCAAGGTGAGAGCTTCTTGTGATCTGATTTCAAGC	1020
QY	1039	TTGTGTGTCGCGCAGAAAGAGAGACTGAATTTGAAGCTCTTGTGTCATCTCTTCTTC	1099

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Db 1081 TCTAAATATGACTGGAACAAATCTTGAATCTCTCCCTCTTCTTCCACCTCAAG 1140
Qy 1159 TCTGAAGATGACACTCCAAATTTTGAATGAACAGAGAAAGAAATTCGTGGGTTTCACTCTC 1218
Db 1141 TCTGAAGATGACACTCCAAATTTTGAATGAACAGAGAAAGAAATTCGTGGGTTTCACTCTC 1200
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Db 1201 CCGTGCACAGCTGAGCCCTCAGGCTTCTCGGCTGAAGAACTGCGTTTGTGGGTTTTCG 1260
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Qy 1519 TCCCTCTGAGAGAGACCTTGTCTACTATCATCAAGAAATGCAATGCTTAAAGCGAAGT 1578
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Db 1621 GATATCAGAGAGAGAGCCGGAAGCTTCAAGAAATCAAGAGAGAGATCCAGGCTCA 1680
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Db 1801 CCGAAAGCGACAGAAATGTCAGATTAATCTGTTGAAGCTTAAGATCAAGGAAGCCTGAA 1860
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Qy 1939 CTCGAGAGAACTGAGAGAGGCT----- 1962
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Qy 1963 -----GCAAG 2010
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Qy 2191 AAAACATGGGAG 2250
Db 2221 AAAACATGGGAG 2280
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Db 2341 AAGGAGACCTGAG 2400
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Db 2941 CTTTCTGAAGCTGATCTGATTAATCAAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5661.4	86.1	6165	4 US-10-028-946-1	Sequence 1, Appl
2	5358	81.5	5877	4 US-10-028-946-3	Sequence 3, Appl
3	1397.8	21.3	1515	4 US-09-804-471A-1	Sequence 1, Appl
4	1397.8	21.3	1515	4 US-10-238-709-1	Sequence 1, Appl
5	965.6	14.7	2162	4 US-09-774-528-419	Sequence 1, Appl
6	768	11.7	1133	4 US-09-916-204-1	Sequence 1, Appl
7	768	11.7	1133	4 US-10-282-048-1	Sequence 1, Appl
8	570	8.7	2188	4 US-09-949-016-2533	Sequence 2533, Ap
9	570	8.7	17455	4 US-09-949-016-14275	Sequence 14275, A
10	373.2	5.7	1398	4 US-09-513-999C-22836	Sequence 29836, A
11	258	3.9	258	4 US-09-016-434-513	Sequence 513, App
12	228.2	3.5	2423	4 US-09-949-016-2640	Sequence 2640, Ap
13	220.8	3.4	2726	2 US-08-422-699A-12	Sequence 12, Appl
14	220.8	3.4	2726	2 US-08-422-706B-12	Sequence 12, Appl
15	214	3.3	2511	2 US-08-422-699A-8	Sequence 8, Appl
16	214	3.3	2511	2 US-08-422-706B-8	Sequence 8, Appl
17	213.6	3.2	3182	1 US-08-484-044-11	Sequence 11, Appl
18	205	3.1	174493	4 US-09-804-471A-3	Sequence 3, Appl
19	205	3.1	174493	4 US-10-238-709-3	Sequence 3, Appl
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21	189.2	2.9	2706	2 US-09-005-069-61	Sequence 61, Appl
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23	189.2	2.9	2706	4 US-09-004-130A-20	Sequence 20, Appl
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44	111.4	1.7	1935	2 US-09-272-796-11	Sequence 11, Appl
45	109.8	1.7	3213	3 US-09-442-100-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/10028946
; Patent No. 6734009
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanhuan
; APPLICANT: Miranda, Marcia
; APPLICANT: Fridde, Carl John
; TITLE OF INVENTION: No. 6734009 Human Kinases and Polynucleotides Encoding the Sam
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-1

Query Match 86.1%; Score 5661.4; DB 4; Length 6165;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 16; Indels 243; Gaps 3;

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DB	61	GCCAGCGGGGCTCCAGGCTGATCTGTTCTTCAAGGGAACAACCTTTATGACTCA	120
QY	139	CAGCAGATCTCTCTTTTCCGAGAGGATATGATGCCCTTTGTTCTTTGAA	198
DB	121	CAGCAGATCTCTCTTTTCCGAGAGGATATGATGCCCTTTGTTCTTTGAA	180
QY	199	GATGATGACGACCTCTCTGATGAGATTAAGCACTGTAAGCACTTTTCCGAGAT	258
DB	181	GATGATGACGACCTCTCTGATGAGATTAAGCACTGTAAGCACTTTTCCGAGAT	240
QY	259	TCCGACACCATAGCTGATTAAGAGAGCTCCAGCTTCGCAAGGACTTCAGAGTCA	318
DB	241	TCCGACACCATAGCTGATTAAGAGAGCTCCAGCTTCGCAAGGACTTCAGAGTCA	300
QY	319	AGCTTTGATGTTGCTGATCTTTGCTGATGAGTGAAGAGAGAGCAACCGGG	378
DB	301	AGCTTTGATGTTGCTGATCTTTGCTGATGAGTGAAGAGAGAGCAACCGGG	360

QY	379	GAAATCTATGCTATGAAAGTGATGAAGAAAGAGCTTTTATTTGGCCAGAGACAGTTTCA	438
Db	361	GAACTCTATGCTATGAAAGTGATGAAGAAAGAGAGCTTTTATTTGGCCAGAGACAGTTTCA	420
QY	439	TTTTTTGAGGAAGAGCGGACATATATATCTCGAAGACAAGGCCCGTGGATCCCGCCAAATTA	498
Db	421	TTTTTTGAGGAAGAGCGGACATATATATCTCGAAGACAAGGCCCGTGGATCCCGCCAAATTA	480
QY	499	CAGTATGCCCTTTGAGGACAAAAATCACCTTTATCTGATGGAGGAATATCAGCTTGAGGG	558
Db	481	CAGTATGCCCTTTGAGGACAAAAATCACCTTTATCTGATGGGAATATCAGCTTGAGGG	540
QY	559	GACTTGCCTGCACTTTTGAATATGATATGAGGACCACTTGTGATGATAAACTGTATCAGTTT	618
Db	541	GACTTGCCTGCACTTTTGAATATGAGGACCACTTGTGATGATAAACTGTATCAGTTT	600
QY	619	TACTAGCTGAGCTGATTTTGGCTGTTTCAACGGTTCATCTGATGGATACGTGATCGA	678
Db	601	TACTAGCTGAGCTGATTTTGGCTGTTTCAACGGTTCATCTGATGGATATCGTGAATCA	660
QY	679	GACATCAAGCCTGAGAAACATTCCTCGTTGACCGGACAGGACATCTCAAGCTGGTGAATTTT	738
Db	661	GACATCAAGCCTGAGAAACATTCCTCGTTGACCGGACAGGACATCTCAAGCTGGTGAATTTT	720
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QY	919	TCCCCCTTTCGAGAGAGGAACCTCTGCGAAGACCTTCAATATGAAATTTCCAGCGG	978
Db	901	TCCCCCTTTCGAGAGAGGAACCTCTGCGAAGACCTTCAATATGAAATTTCCAGCGG	960
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; APPLICANT: Yu, Xuechuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fridele, Carl Johan
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028, 946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-3

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; Sequence 1, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCES: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Human
US-09-804-471A-1
Query Match 21.3%; Score 1397.8; DB 4; Length 1515;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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US-10-238-709-1
; Sequence 1, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CD001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
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NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Human
US-10-238-709-1

Query Match      21.3%; Score 1397.8; DB 4; Length 1515;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 661 CATCGAGACATCAAGCTTGAGAACATTCCTGTTACCGACAGAGACATCAAGCTGTG 720
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QY 733 GATTTTGAATCTGCGCGGAAATGAAATTTGAAACAAATAGTGAAATGCCAAATCCCGATT 792
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    |||
Db 721 GATTTTGAATCTGCGCGGAAATGAAATTTGAAACAAATAGTGAAATGCCAAATCCCGATT 780
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QY 793 GGGAGCCCAAGATTACATGAGCTCTGAAAGTCTGACCTGATGAAACGGGATGGAAAAGGC 852
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    |||
Db 781 GGGAGCCCAAGATTACATGAGCTCTGAAAGTCTGACCTGATGAAACGGGATGGAAAAGGC 840
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    |||
QY 853 ACCTACGAGCTGAGCTGTGACCTGTGATCACTGAGGCTGATGCTTATGATGATTTAT 912
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    |||
Db 841 ACCTACGAGCTGAGCTGTGACCTGTGATCACTGAGGCTGATGCTTATGATGATTTAT 900
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QY 913 GGGAGATCCCTTCCGAGAGGGAACCTTCCAGAAACCTTCAATTAATTAATTTTC 972
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Db 901 GGGAGATCCCTTCCAGAGGGAACCTGCGCAGAACTCTCATTAACATTAATGATTTTC 960
Qy 973 CAGCGGTTTTGAATTTCCAGATGACCCCAAGTGAAGACGACTTTCTTGATCTGATTT 1032
Db 961 CAGCGGTTTTGAATTTCCAGATGACCCCAAGTGAAGACGACTTTCTTGATCTGATTT 1020
Qy 1033 CAAAGCTTGTTGGGGCCAGAAAGAGACCTGAAGTTTGAAGTCTTTGCTGCGCATTCCT 1092
Db 1021 CAAAGCTTGTTGGGGCCAGAAAGAGACCTGAAGTTTGAAGTCTTTGCTGCGCATTCCT 1080
Qy 1093 TTCTTCTAAATTTAGCTGGAACAACATTCGTAATCTCTCCCTCTGTTCCACCC 1152
Db 1081 TTCTTCTAAATTTAGCTGGAACAACATTCGTAATCTCTCTCCCTCTGTTCCACCC 1140
Qy 1153 CTCAGCTGACGATGACACCTTCAAATTTTGATGAACGAGAGAAATTCGCGGTTTCA 1212
Db 1141 CTCAGCTGACGATGACACCTTCAAATTTTGATGAACGAGAGAAATTCGCGGTTTCA 1200
Qy 1213 TCCTCTCGGTCGAGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGGGG 1272
Db 1201 TCCTCTCGGTCGAGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGGGG 1260
Qy 1273 TTTTCGTAGACGAGGACCTGCGGATTTCTGTAGATCTGAGTCTGTGTGTCGGGTCG 1332
Db 1261 TTTTCGTAGACGAGGACCTGCGGATTTCTGTAGATCTGAGTCTGTGTGTCGGGTCG 1320
Qy 1333 GACTCCCTGCCAAGCACTGAGCTCCATGAGAAAGAACTTCTCATCAAAAGCAAGCTA 1392
Db 1321 GACTCCCTGCCAAGCACTGAGCTCCATGAGAAAGAACTTCTCATCAAAAGCAAGCTA 1380
Qy 1393 CAAGACTCTCAGGACGAGTGTCAAGAT 1421
Db 1381 CAAGACTCTCAGGACGAGTGTCAAGAT 1409

RESULT 5

US-09-774-528-419
Sequence 419, Application US/09774528
Patent No. 6743619
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Zhao, Qing A.
APPLICANT: Yang, Yonghong
APPLICANT: Xue, Aidong J.
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: Drmanac, Radote T.
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
FILE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pf_genes Version 2.0
SEQ ID NO 419
LENGTH: 2162
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (364)..(2010)
US-09-774-528-419

Query Match 14.7%; Score 965.6; DB 4; Length 2162;
Best Local Similarity 99.1%; Pred. No. 1.8e-264;

Matches 971; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 AGAGCCGCGAGTGGGAGATGTTGAAGTTCAATATGAGCCCGGAATCTTTGGATGCT 60
Db 346 AATGCGCCAGTGGGAGATGTTGAAGTTCAATATGAGCCCGGAATCTTTGGATGCT 405
Qy 61 GGTGCTGTAACCAATTCGAGCGGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAA 120
Db 406 GGTGCTGTAACCAATTCGAGCGGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAA 465
Qy 121 CCACCTTTATGACTCAACAGAGATGTCCTCTTTTCCGAGAAAGGATATTAATGTC 180
Db 466 CCACCTTTATGACTCAACAGAGATGTCCTCTTTTCCGAGAAAGGATATTAATGTC 525
Qy 181 CTCTTGTCTCTTTGAAGAAATGCAATGCTGCTCTGATGAATTAAGACGTAAC 240
Db 526 CTCTTGTCTCTTTGAAGAAATGCAATGCTGCTCTGATGAATTAAGACGTAAC 585
Qy 241 AACTTGTCCGAGATTCGAGACATAGCTGAGTTACAGAGCTCCAGCTTCGGA 300
Db 586 AACTTGTCCGAGATTCGAGACATAGCTGAGTTACAGAGCTCCAGCTTCGGA 645
Qy 301 AAGACTTGAAGTCAAGATCTGTAGGTTGTGTCATTTGCTGAAGTGAAGTGA 360
Db 646 AAGACTTGAAGTCAAGATCTGTAGGTTGTGTCATTTGCTGAAGTGAAGTGA 705
Qy 361 AAGAGAAAGCAACCGGGACATCTATGCTATGAAGTGAAGAAAGGCTTTATTTG 420
Db 706 AAGAGAAAGCAACCGGGACATCTATGCTATGAAGTGAAGAAAGGCTTTATTTG 765
Qy 421 GCCAGAGACAGATTTCAATTTTGAAGAAAGCGGAAACATTTATCTGAAGCAAGC 480
Db 766 GCCAGAGACAGATTTCAATTTTGAAGAAAGCGGAAACATTTATCTGAAGCAAGC 825
Qy 481 CCGTGAATCCCAATTAACAGATGCTTTCAAGACAAAAATCACCTTTATCTGATGAG 540
Db 826 CCGTGAATCCCAATTAACAGATGCTTTCAAGACAAAAATCACCTTTATCTGATGAG 885
Qy 541 GAATATCAGCTGAGGGGACCTTGCTGTCATTTTGAATGATATGAGGACCAATTAGT 600
Db 886 GAATATCAGCTGAGGGGACCTTGCTGTCATTTTGAATGATATGAGGACCAATTAGT 945
Qy 601 GAAACCTGATCAGTTTAACTAGCTGAGCTGATTTTGGCTTCAAGGCTTATCTG 660
Db 946 GAAACCTGATCAGTTTAACTAGCTGAGCTGATTTTGGCTTCAAGGCTTATCTG 1005
Qy 946 GAAACCTGATCAGTTTAACTAGCTGAGCTGATTTTGGCTTCAAGGCTTATCTG 1005
Db 661 ATGGATACGTCATCGAGACATCAAGCTTGAAACATTTCTGTTGACCGCACAGACAC 720
Qy 1006 ATGGATACGTCATCGAGACATCAAGCTTGAAACATTTCTGTTGACCGCACAGACAC 1065
Db 721 ATCAAGCTGTGATTTTGAATCTGCTGCGGAAATGAATTCAAACAGATGTAATGCC 780
Qy 1066 ATCAAGCTGTGATTTTGAATCTGCTGCGGAAATGAATTCAAACAGATGTAATGCC 1125
Db 781 AAACCTCGGATTTGGAACCCAGATTAACATAGCTTCCGAAGTCTGATGTAAGCGGG 840
Qy 1126 AAACCTCGGATTTGGAACCCAGATTAACATAGCTTCCGAAGTCTGATGTAAGCGGG 1185
Db 841 GATGAAAAAGCACCTGAGCTGAGCTGATGCTGTGCTAGTGGGCTGATTCCTAT 900
Qy 1186 GATGAAAAAGCACCTGAGCTGAGCTGATGCTGTGCTAGTGGGCTGATTCCTAT 1245
Db 901 GATGATTTTATGAGGATTCCTCTTCCAGAGGAACTCTGCGCAACCTTCAATTAAC 960
Qy 1246 GATGATTTTATGAGGATTCCTCTTCCAGAGGAACTCTGCGCAACCTTCAATTAAC 1305
Db 961 ATTATGAATTTCCAGGTT 980
Qy 1306 ATTATGAATTTCCAGGTT 1325
Db

RESULT 6

US-09-916-204-1

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/ Sequence 1, Application US/09916204
/ Patent No. 6638745
/ GENERAL INFORMATION:
/ APPLICANT: WEI, Ming-Hui et al.
/ TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: CL001164CIP
/ CURRENT APPLICATION NUMBER: US/09/916,204
/ CURRENT FILING DATE: 2001-07-24
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 1133
/ TYPE: DNA
/ ORGANISM: Human
US-09-916-204-1
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Query Match 11.7%; Score 768; DB 4; Length 1133;
Best Local Similarity 99.4%; Pred. No. 3.1e-208;
Matches 771; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 1 AGAGCCGCCAGTGGGAGATGTTGAAGTCAATATATGAGCGGGAATCCTTTGATGCT 60
DB 36 AGAGCCGCCAGTGGGAGATGTTGAAGTCAATATATGAGCGGGAATCCTTTGATGCT 95
QY 61 GGTGCTGTGAACCCATTGCGACCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAA 120
DB 96 GGTGCTGTGAACCCATTGCGACCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAA 155
QY 121 CGACCCCTTATGACTCAACAGCAGATGTCCTCTTCCGAGAAAGGATTTAGATGCC 180
DB 156 CCACCCCTTATGACTCAACAGCAGATGTCCTCTTCCGAGAAAGGATTTAGATGCC 215
QY 181 CTCTTGTCTCTTTGAGAATGCAAGTCAAGCTGCTCTGATGAAGATTAAGCACTGAGC 240
DB 216 CTCTTGTCTCTTTGAGAATGCAAGTCAAGCTGCTCTGATGAAGATTAAGCACTGAGC 275
QY 241 AACTTTGTCCGGAAGTATTCGACACCATAGCTGATGATGATGATGATGATGATGATG 300
DB 276 AACTTTGTCCGGAAGTATTCGACACCATAGCTGATGATGATGATGATGATGATGATG 335
QY 301 AAGGACTTCGAAAGTCAAGATGCTTTGAGAGTGAAGTGAAGAAAGGCTTTATTTG 360
DB 336 AAGGACTTCGAAAGTCAAGATGCTTTGAGAGTGAAGTGAAGAAAGGCTTTATTTG 395
QY 361 AGAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTGAAGAAAGGCTTTATTTG 420
DB 396 AGAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTGAAGAAAGGCTTTATTTG 455
QY 421 GCCCAGAGCAGGTTTATTTTGAAGAGAGCGGAACATATTTATCTGAAACACAAGC 480
DB 456 GCCCAGAGCAGGTTTATTTTGAAGAGAGCGGAACATATTTATCTGAAACACAAGC 515
QY 481 CCGTGATCCCCCAATTACAGTATGACCTTTCAGGACAAAATCACCTTATCTGATGAG 540
DB 516 CCGTGATCCCCCAATTACAGTATGACCTTTCAGGACAAAATCACCTTATCTGATGAG 575
QY 541 GAATATCAGCTCGAGGGGACTTGCTGCTCACTTTTGAATAGATATGAGCAAGTTAGAT 600
DB 576 GAATATCAGCTCGAGGGGACTTGCTGCTCACTTTTGAATAGATATGAGCAAGTTAGAT 635
QY 601 GAAAACTGATACGTTTATCTAGCTGAGCTGATTTTGGCTGTTCAACGCTTCATCTG 660
DB 636 GAAAACTGATACGTTTATCTAGCTGAGCTGATTTTGGCTGTTCAACGCTTCATCTG 695
QY 661 ATGGGATACGTCATCGAGCATCAAGCTGAGAACTTCTGTTGACCGACAGGACAC 720
DB 696 ATGGGATACGTCATCGAGCATCAAGCTGAGAACTTCTGTTGACCGACAGGACAC 755
QY 721 ATCAAGCTGTGATTTTGGATCTGCGCGGAAAATGAATTCAAACAAGATGTTGAA 776
DB 756 ATCAAGCTGTGATTTTGGATCTGCGCGGAAAATGAATTCAAACAAGATGTTGAA 811
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RESULT 7
US-10-282-048-1
/ Sequence 1, Application US/10282048
/ Patent No. 6692948
/ GENERAL INFORMATION:
/ APPLICANT: WEI, Ming-Hui et al.
/ TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: CL001164CIP-DIV
/ CURRENT APPLICATION NUMBER: US/10/282,048
/ CURRENT FILING DATE: 2002-10-29
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 1133
/ TYPE: DNA
/ ORGANISM: Human
US-10-282-048-1
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Query Match 11.7%; Score 768; DB 4; Length 1133;
Best Local Similarity 99.4%; Pred. No. 3.1e-208;
Matches 771; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 1 AGAGCCGCCAGTGGGAGATGTTGAAGTCAATATATGAGCGGGAATCCTTTGATGCT 60
DB 36 AGAGCCGCCAGTGGGAGATGTTGAAGTCAATATATGAGCGGGAATCCTTTGATGCT 95
QY 61 GGTGCTGTGAACCCATTGCGACCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAA 120
DB 96 GGTGCTGTGAACCCATTGCGACCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAA 155
QY 121 CGACCCCTTATGACTCAACAGCAGATGTCCTCTTCCGAGAAAGGATTTAGATGCC 180
DB 156 CCACCCCTTATGACTCAACAGCAGATGTCCTCTTCCGAGAAAGGATTTAGATGCC 215
QY 181 CTCTTGTCTCTTTGAGAATGCAAGTCAAGCTGCTCTGATGAAGATTAAGCACTGAGC 240
DB 216 CTCTTGTCTCTTTGAGAATGCAAGTCAAGCTGCTCTGATGAAGATTAAGCACTGAGC 275
QY 241 AACTTTGTCCGGAAGTATTCGACACCATAGCTGATGATGATGATGATGATGATGATG 300
DB 276 AACTTTGTCCGGAAGTATTCGACACCATAGCTGATGATGATGATGATGATGATGATG 335
QY 301 AAGGACTTCGAAAGTCAAGATGCTTTGAGAGTGAAGTGAAGAAAGGCTTTATTTG 360
DB 336 AAGGACTTCGAAAGTCAAGATGCTTTGAGAGTGAAGTGAAGAAAGGCTTTATTTG 395
QY 361 AGAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTGAAGAAAGGCTTTATTTG 420
DB 396 AGAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTGAAGAAAGGCTTTATTTG 455
QY 421 GCCCAGAGCAGGTTTATTTTGAAGAGAGCGGAACATATTTATCTGAAACACAAGC 480
DB 456 GCCCAGAGCAGGTTTATTTTGAAGAGAGCGGAACATATTTATCTGAAACACAAGC 515
QY 481 CCGTGATCCCCCAATTACAGTATGACCTTTCAGGACAAAATCACCTTATCTGATGAG 540
DB 516 CCGTGATCCCCCAATTACAGTATGACCTTTCAGGACAAAATCACCTTATCTGATGAG 575
QY 541 GAATATCAGCTCGAGGGGACTTGCTGCTCACTTTTGAATAGATATGAGCAAGTTAGAT 600
DB 576 GAATATCAGCTCGAGGGGACTTGCTGCTCACTTTTGAATAGATATGAGCAAGTTAGAT 635
QY 601 GAAAACTGATACGTTTATCTAGCTGAGCTGATTTTGGCTGTTCAACGCTTCATCTG 660
DB 636 GAAAACTGATACGTTTATCTAGCTGAGCTGATTTTGGCTGTTCAACGCTTCATCTG 695
QY 661 ATGGGATACGTCATCGAGCATCAAGCTGAGAACTTCTGTTGACCGACAGGACAC 720
DB 696 ATGGGATACGTCATCGAGCATCAAGCTGAGAACTTCTGTTGACCGACAGGACAC 755
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RESULT 10
US-09-513-999C-29836/C
; Sequence 29836, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, J.Y.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 29836
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 119
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 121
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 124
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 125
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 130
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 136
; OTHER INFORMATION: h=a or c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 138
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 252
; OTHER INFORMATION: s=g or c
US-09-513-999C-29836

Query Match
Best Local Similarity 5.7%; Score 373.2; DB 4; Length 398;
Matches 384; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

Db 6138 GCAGCAGGTTGAAAGTCTGTCTGAGACAGATTATTTGAGAGAGTTCACTGAGT 6197
398 GCAGCAGGTTGAAAGTCTGTCTGAGACAGATTATTTGAGAGAGTTCACTGAGT 339

Qy 6198 TCTAGACGTGTGACTTAAATAATGAGCTTAAAGCTGAGAGCCAGCCACTGCTTAC 6257
338 TCTAGACGTGTGACTTAAATAATGAGCTTAAAGCTGAGAGCCAGCCACTGCTTAC 279

Db 6258 AAAAGAGTCTTAAATGAGAGTGTGAAGAAATTTGAAACCTCATCTGAATC 6317
278 AAAAGAGTCTTAAATGAGAGTGTGAAGAAATTTGAAACCTCATCTGAATC 219

Qy 6318 AGAAGCTTAAATTTCTATGAATGACACTCCCTGAGAGCCGAGAGCAATCTGTGT 6377
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Db 218 AGAAGCTTAAATTTCTATGAATGACACTCCCTGAGAGCCGAGAGCAATCTGTGT 159
Qy 6378 TGAATTTGAGAGCAGGCAAG--ACCAACACTGTATTTAGTTCCATGCCAGGCTCAAC 6435
158 TGAATTTGAGAGCAGGCAAGSADCCACACCTGAGTTTAACTTCAATGAGGCTCAAC 99

Qy 6436 AGGACCAAGTGGCTGGCTTAAATAACACACAGATGAGAAATGATGTGGCTCAGT 6495
98 AGGACCAAGTGGCTGGCTTAAATAACACACAGATGAGAAATGATGTGGCTCAGT 39

Qy 6496 CCTGTTCCTCCAGATTTTATCTGGAAGAGTTGCA 6533
38 CCTGTTCCTCCAGATTTTATCTGGAAGAGTTGCA 1

Db 38 CCTGTTCCTCCAGATTTTATCTGGAAGAGTTGCA 1

RESULT 11
US-09-016-434-513
; Sequence 513, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 513:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 258 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINON01
; CLONE: 2290031
US-09-016-434-513

Query Match
Best Local Similarity 3.9%; Score 258; DB 4; Length 258;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5069 GCAAAGTCGTCATCTCCGCTACAGAAACCTGAGCAATCTGATCCGGAAGAG 5128
1 GCAAAGTCGTCATCTCCGCTACAGAAACCTGAGCAATCTGATCCGGAAGAG 60

Db 5129 TAGAGCTGAGAGCCCTGAGCTGATCACTTCACAATTAACATATCTATTGAA 5188
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Db 61 TAGAGACTCAGACCCCTGAGCTGTATCCATTGACCAATTACAGATATCTCATTTGAA 120
Qy 5189 CCAATAAATTTCTACGAAATTCGACATGAGACATGACATCGCTCGAGAAATTCCTGGATTAAGA 5248
Db 121 CCAATAAATTTCTACGAAATTCGACATGAGACATGACATCGCTCGAGAAATTCCTGGATTAAGA 180
Qy 5249 ATGACATTCCTTGGACCTGTGTGTGGCCGCTCTTCGACAGCTTCCCTGTCTCAA 5308
Db 181 ATGACATTCCTTGGACCTGTGTGTGGCCGCTCTTCGACAGCTTCCCTGTCTCAA 240
Qy 5309 TCGTGAGGTGAACAGCG 5326
Db 241 TCGTGAGGTGAACAGCG 258
RESULT 12
US-09-949-016-2640
; Sequence 2640, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VERTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2640
; LENGTH: 2423
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-2640
Query Match 3.5%; Score 228.2; DB 4; Length 2423;
Best Local Similarity 52.2%; Pred. No. 8.9e-54;
Matches 587; Conservative 0; Mismatches 523; Indels 15; Gaps 3;
Qy 170 TATTAGATGCGCTCTTGTCTTCTTGAAGATGACGTCAGCTGCTGTGATGAATTA 229
Db 1021 TACTGATATACCTATCTGCTTATGATGAATGCAATATCTCCATTGAGAGAGAGA 1080
Qy 230 AGCAGGTGAGCACTTGTCCGGAATATCCGACACCAATAGCTGATACAGAGACTCC 289
Db 1081 AGAACAATCTCGAATACCTAAGATGAGGCTAAACCAATTTACTTAAAGTGAACAAATGC 1140
Qy 290 AGCCTTCGCGAAGAGCTTGAAGTGAAGTCTTGAAGTGTGCTGCTGCTGAAG 349
Db 1141 GATTCATAGAGAGAGCTTGAATATTAAGTGATGTGCTGAGAGAGCTTTGGGAGG 1200
Qy 350 TCGAGGTGTAAG 409
Db 1201 TGTGTGTATGTAAG 1260
Qy 410 AGGCTTTATTTGGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 469
Db 1261 GGAAGAAATGCTGAAG 1320
Qy 470 GAAGCAAG 529
Db 1321 ATGAG 1380
Qy 530 ATCTGATGAG 589
Db 1381 ACCTGCTTATGAG 1440
Qy 590 ACCAGTATATGAG 649

Db 1441 ATAGATGCTCAGAGATATGCTAGATTTTACTTGGCTGAGATGATGATGATGACT 1500
Qy 650 GCGTTCATGTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 709
Db 1501 CAGTTCATGCTATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
Qy 710 GAG 769
Db 1561 TGAATGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Qy 770 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 829
Db 1621 CGGTTCATGCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Qy 830 TATGAG 889
Db 1681 CCATGAGAG--ATGAG 1737
Qy 890 TGAATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 949
Db 1738 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1797
Qy 950 CTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1006
Db 1798 CATGAG 1857
Qy 1007 TGAG 1064
Db 1858 TGTGAG 1917
Qy 1065 -----GAGTTGAG 1117
Db 1918 GTCAAAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1977
Qy 1118 ACATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1177
Db 1978 ATATTCGAG 2037
Qy 1178 ATTTGATGAG 1237
Db 2038 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2097
Qy 1238 CAGGCTTCGAG 1282
Db 2098 CTGCAATTTCTGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2142
RESULT 13
US-08-422-699A-12
; Sequence 12, Application US/08422699A
; Patent No. 5955265
; GENERAL INFORMATION:
; APPLICANT: Brook, J. David
; APPLICANT: Houseman, David B.
; APPLICANT: Shaw, Duncan J.
; APPLICANT: Harley, Helen G.
; APPLICANT: Johnson, Keith J.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
; DYSTROPHY GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,699A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-422-699A-12

Query Match 3.4%; Score 220.8; DB 2; Length 2726;
Best Local Similarity 53.7%; Pred. No. 1.3e-51;
Matches 531; Conservative 0; Mismatches 442; Indels 15; Gaps 3;
QY 212 CTGCTCTGTAAGATTAGACGCTGAGCACTTTGTCCGAAAGTATTCGACACCATAG 271
DB 243 CCGAATCTGGCCAGAGCAAGTACGTGGCCGACTTCTTGAGTGGCCGAGCCCATCTGG 302
QY 272 CTGAGTTACAGAGCTCCAGCTTCGCGCAAGGACTTGGAATCAGAACTTTGAGTT 331
DB 303 TGAGGCTTAAGAGAGCTCCGACTGCGAGAGGACGACTTCAAGATTCGAAAGTGATCGAC 362
QY 332 GTGTCTACTTTGCTGAAGTGAAGTGTGAAGAGAAAGCAACCGGGGACATCTATGCTA 391
DB 363 GCGGGGCGTTACGACGAGTACGCGTATGTAAGATGAAAGACGCGGCCAGGTATGCA 422
QY 392 TGAAGTGTGAAGAAGAGGCTTATATGGCCACAGAGAGGTTTCATTTTGAAGAG 451
DB 423 TGAAGATCATGAACAAGTGGACATGCTGAAGAGGCGAGGTGTGCTTCCCTGAGG 482
QY 452 AGCGGAATATTTATCTCGAAGACACAGCCCGTGGATCCCCCAATTAAGATAGCTTTC 511
DB 483 AGAGGAGCGTGTGGTGAATGGGACCGCGGTGATACGAGCTGACCTTCGCTTCC 542
QY 512 AGGACAAAATACCTTTATCTGATGAGAAATATCAGCTGAGAGGAGCTTGTCTCAC 571
DB 543 AGAAGAAATACCTGTAACCTGTCATGAGTATTAAGTGGCGGGGACCTGCTGACAC 602
QY 572 TTTTGAATAGATATGAGCCAGCTAGATGAAGAAAACCTGATACAGTTTAACTAGTGA 631
DB 603 TGCTGAGCAAGTTTGGGAGCGGATTCGCGCGAAGTGGCGGCTTCTTACCTGGCGAGA 662
QY 632 TGAATTTGGCTTTCACAGCGCTTCACTGATGGAGTACGTGCATCGAGACATCAAGCCTG 691
DB 663 TTGTATGCGCATAGACTCGGTGACCGGCTTGGCTTACGTGCAAGGAGCATCAAAACCG 722

QY 692 AAGAACTTCTGTTAGCCGACAGACATCAAGCTGTGTGATTTGGATCTGCCGGA 751
DB 723 ACAACATCTCTGAGACGCTGTGGCACATCTCGCTGGCCGACTTCCGCTTGGCTCA 782
QY 752 AATGAAATCAACAAGATGTGAATGCAACTCCGATTTGGACCCCAATTACATGG 811
DB 783 AGCTGGGCGAATGAAACGCTGCGCGTGTGTGTGTGTGGCACCCCACTACCTGT 842
QY 812 CTCCTGAAGTCTGA---CTGTATGAACGGGATGAAAAAGCACCTACGGCTGAGCT 868
DB 843 CCCCCGAGATCTTGAGAGCTGTGGCGGTGGCCCTGGAGACAGACGCTACGGCCGAGT 902
QY 869 GTGACTGTGTGCTGATGAGCGCTGATGCTTATGATATTTATGAGAGATCCCTTTCG 928
DB 903 GTGACTGTGTGGCGCTGGGTGTATTCGCTTATGAATGTCTATGAGGACAGCCCTTCT 962
QY 929 CAGAGGAACCTCTGCCGAACCTTCATTAATTAATTTCCAGGCGTTTGAAT 988
DB 963 AGCGGAATTCACGCGGAGACCTATGCGAAGATGCTCACTACAAAGAGCACTCTCTC 1022
QY 989 TTCCAGATGACCCCAAGTGAAGTGAAGT---GACTTCTGTATCTGATTCGAAGTGTGT 1045
DB 1023 TGCCGCTGTGTGAGAGAGGGGTCCCTGAGAGGCTCGAGACTTACAGCGGTGTGCT 1082
QY 1046 GCGGCTCAAAAGAGACTGAAGTTTGAAGTCTTTGCTG-----CATCTTCT 1096
DB 1083 GTCCCCGAGACACAGCTGGGCGGGGTGAGAGCGGCACTTCGACACATCCCTCT 1142
QY 1097 TCTTAAATTTAGCTGAAACAACATTCGTAATCTCCCTCCCTGGTGTCCACCCCTCA 1156
DB 1143 TCTTTGGCTGCTGATCGGATGTGTCTCCGGACACAGCGTCCCTTTACACCGAATTCG 1202
QY 1157 AGTCTGACGATGACACTCCAAATTTGA 1184
DB 1203 AAGGTGCCACCGACATGCAACTTGA 1230

RESULT 14
US-08-422-706B-12
Sequence 12, Application US/08422706B
GENERAL INFORMATION:
PATENT No. 5977333
APPLICANT: Brook, J. David
APPLICANT: Houseman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen G.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA: PCT/US93/01545
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA: PCT/GB93/00253
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA: GB9202485.0
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-422-7068-14

Query Match 3.4%; Score 220.8; DB 2; Length 2726;
Best Local Similarity 53.7%; Pred. No. 1.3e-51;
Matches 531; Conservative 0; Mismatches 442; Indels 15; Gaps 3;

212 CTGCTGTGATGAGATTAGACGATGAGCACTTTGTCGCGAAGTATCCGACACCATG 271
243 CCCAATCGGCCGAGCAAGTACGTGCGCATCTTGTGCGAGCGGAGCCCATGCTG 302
272 CTGAGTTACAGAGCTCCAGCCTTCGCAAGGACTTCAGAGTCTTGAAGTT 331
303 TGAGGCTTAAGAGAGTCCGCTGCAAGAGGACGACTTCGAGATTCGAGATCGGAC 362
332 GTGCTCATTTGCTGAAGTGTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 391
363 GCGGGCGTTCAACGAGGTGAGGTGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAG 422
392 TGAAGTGAAG 451
423 TGAAGTGAAG 482
452 AGCGAACAATATATCTCGAAGCAAGCCGTCGATCCCGCAATTACAGTATGCTTTC 511
483 AGAGGAGAGTGTGAGAGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542
512 AGGACAAAATACCTTTATCTGATGAGAGATATACAGCTGAGAGAGAGAGAGAG 571
543 AGGATGAGAACTACCTGATCTGATGAGAGATATACAGCTGAGAGAGAGAGAG 602
572 TTTTGAATGATGAG 631
603 TGTGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 662
632 TGATTTGCTGTTTCAAGAGCTTCATCTGATGAGAGATACGTCAGAGATCAAGCTTC 691
663 TTCTCATGCGCAATGAGATCGGTGACAGCGCTTGGCTACGTCAGAGAGATCAAG 722
692 AGAACAATCTGTTGAG 751
723 ACAACATCTGAG 782
752 AATGAATTCAG 811
783 AGCTGCGGAG 842
812 CTCCTGAAGTGTGA---CTGTGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 868
843 CCCCCGAGATCTGAG 902

869 GTGACTGTGTGTCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 928
903 GTGACTGTGTGTCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 962
929 CAGAGGAACTCTGTCAG 988
963 ACCGGAATTCACAGGAG 1022
989 TTCAGATGACCCCAAGTGTGAGAGT---GACTTCTGATCTGATTAAGAGTGTGT 1045
1023 TGCCTGTGTGAG 1082
1046 GCGGCGAG 1096
1083 GTCCCGGAG 1142
1097 TCTCTAAATTTGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1156
1143 TCTTTGCTCTGAG 1202
1157 AGCTGAG 1184
1203 AAGGTCCAG 1230

RESULT 15
US-08-422-699A-8
Sequence 8, Application US/08422699A
Patent No. 5955265
GENERAL INFORMATION:
APPLICANT: Brook, J. David
APPLICANT: Housman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen G.
APPLICANT: Johnson, Keith J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,699A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992

```
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1746
US-08-422-699A-8
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Query Match 3.3%; Score 214; DB 2; Length 2511;
Best Local Similarity 54.2%; Pred. No. 1e-49;
Matches 508; Conservative 0; Mismatches 415; Indels 15; Gaps 3;

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QY 262 GACACCATAGCTGAGTTACAGAGCTCCAGCCTTCGCAAGGACTTCGAAGTCAGAGT 321
DB 43 GCCATCGTGAGGAGCTTAAGAGAGTCCGACATGACAGAGGAGACGACTTCGAGATTCTGAAG 102
QY 322 CTGTGAGTTGTGTGATCACTTGTCTGAAGTCAGAGTGTGAAGAGAACACCGGGGAC 381
DB 103 GTGATCGAGCGGGGGCGTTCAAGCGGTAGCGGTAGTGAAGTGAAGCAGAGCGGCCAG 162
QY 382 ATCTATGCTATGAAAGTGTGAAGAGAGAGGCTTTATTGCGCCAGAGCAGGTTTCATTT 441
DB 163 GTGTATGTCATGAGATCATGAAACAGTGGGACATCTGAAGAGGGCGAGGTGTGTGC 222
QY 442 TTTGAGAGAGCGGAACTATTATCTCGAAGCACAAGCCGTGATCCCAATTACAG 501
DB 223 TTCGGAGAGAGAGGAGCGTTGTGTAATGGGACCGGCGGTGATCAGCAGCTGCAC 282
QY 502 TATGCTTTCAAGACAAATACACCTTTATCTGATGAGAGAAATATAGCCTGAGAGGAC 561
DB 283 TTGGCTTTCAGAGATGAGACTACCTGTACTGTGTATGAGATATTAAGTGGCGGGAC 342
QY 562 TTGCTGTCACTTTTGAATGATATGAGACCAAGTTAGTGAATGAATCCTGATACAGTTTAC 621
DB 343 CTGCTGACACTGCTGAGCAAGTTGGGAGCGGATTCGGCCGAGATGCGCGCTTCTAC 402
QY 622 CTAGCTGAGCTATTTTGGCTGTTCACAGCGTTCACTGATGAGATACGTGCATCGAGAC 681
DB 403 CTGGCGGAGATTGTCAATGCGCATAGCTCGTGACCGGCTTGCTAGCTGACAGGGAC 462
QY 682 ATCAAGCCTGAGAACATCTCGTTGACCGGACAGACACATCAAGCTGTGATTTTGA 741
DB 463 ATCAAAACCGAACAATCTCTGCTGAGACGCTGTGGCCACATCGCTGTGCGCACTTCGGC 522
QY 742 TCTGCCGCAAAATGATTAACAAGATGTGAATGCCAACTCCCGATTGGACCCCA 801
DB 523 TCTTGCTCAAGCTGCGGCAATGAAAGGTGCGGTGCTGTGGCTGTGGCAACCCA 582
QY 802 GATTACATGGCTCTGGA--AGTCTGACTGTGATGAACGGGGATGAAAAGGCACTTAC 858
DB 583 GACTACTGTCTCCCGAGATCTCTGCGAGGCTGTGGGCGGTGGGCTGGGACAGGCACTAC 642
QY 859 GGCCTGGACTGATGATGCTGTGTGCAAGTGGGCGGTGATGCTATGAGATGTTATGGAGA 918
DB 643 GGGGCCGAGTGTGACTGTGGGCGCTGGGTGTATTCGCTATGAATGTTCTATGGGCGAG 702
QY 919 TCCCCCTTCGACAGAGGAACTCTGCGCAGAACCTTCAATTAACATTATGAAATTTCCAGCGG 978
DB 703 ACGCCCTTCTAGCGGATTTCCAGCGGCGAGACTTATGGCAAGATGCTCACTACAGAGAG 762
QY 979 TTTTGAATTTCCAGATGACCCCAAGTGAACAGT--GACTTCTTGATCTGAATTCAA 1035
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DB 763 CACTCTCTCTGCGCGCTGGTGGACGAGAGGGGTCCCTGAGAGAGGCTCGAGACTTCAATTGAC 822
QY 1036 AGCTTGTGTGCGGCGCCAGAAAGAGACTGAAGTTTGAAGTCTTTGCTGC----- 1086
DB 823 CGGTGCTGTGTCCCGGAGACACGGCTGGGCCGGGGTGGAGCAGCGGACTTCCGAGCA 882
QY 1087 CATCCTTCTCTCTAATAATTGACTGAAACAACATTCGTAACCTCTCTCCCGCCTTCTGTT 1146
DB 883 CATCCTTCTTCTTTTGGCCTGACTGGAGATGCTCTCCGGACAGCGTGCCTCTTTTACA 942
QY 1147 CCCACCTCAAGCTGACGATGACACCTTCAATTTTGA 1184
DB 943 CCGAATTCGAAGGTGCCACCGACACATGCAACTTGA 980
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Search completed: March 2, 2005, 17:05:10
Job time : 962.599 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2005, 10:30:48 ; Search time 893.401 Seconds
(without alignments)
11280.299 Million cell updates/sec

Title: US-10-017-216-3

Perfect score: 6159
Sequence: 1 acgttcgaactcaaatatg.....ttctgagacagatctatgc 6159

Scoring table: IDENTITY_NTC
Gapop 10.0 ; Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5661.4	91.9	6165	4 US-10-028-946-1	Sequence 1, App1
2	5358	87.0	5877	4 US-10-028-946-3	Sequence 3, App1
3	1391.8	22.6	1515	4 US-09-804-471A-1	Sequence 1, App1
4	1391.8	22.6	1515	4 US-10-238-709-1	Sequence 1, App1
5	952.4	15.5	2162	4 US-09-774-528-419	Sequence 1, App
6	750	12.2	1133	4 US-09-916-204-1	Sequence 1, App1
7	750	12.2	1133	4 US-10-282-048-1	Sequence 1, App1
8	258	4.2	258	4 US-09-016-434-513	Sequence 513, App
9	228.2	3.7	2423	4 US-09-949-016-2640	Sequence 2640, App
10	220.8	3.6	2726	2 US-08-422-699A-12	Sequence 12, App1
11	220.8	3.6	2726	2 US-08-422-706B-12	Sequence 12, App1
12	214	3.5	2511	2 US-08-422-699A-8	Sequence 8, App1
13	214	3.5	2511	2 US-08-422-706B-8	Sequence 8, App1
14	213.6	3.5	3182	4 US-08-484-044-11	Sequence 11, App1
15	205	3.3	174493	4 US-09-804-471A-3	Sequence 3, App1
16	205	3.3	174493	4 US-10-238-709-3	Sequence 3, App1
17	189.2	3.1	2706	2 US-08-630-822A-61	Sequence 61, App1
18	189.2	3.1	2706	2 US-09-005-069-61	Sequence 61, App1
19	189.2	3.1	2706	3 US-09-171-156A-20	Sequence 20, App1
20	189.2	3.1	2706	4 US-09-004-730A-20	Sequence 20, App1
21	189.2	3.1	2706	4 US-08-981-799A-20	Sequence 20, App1
22	181.2	2.9	4363	2 US-08-685-576-5	Sequence 295, App
23	179.6	2.9	4888	4 US-09-976-594-295	Sequence 295, App
24	178.8	2.9	48763	4 US-09-916-204-3	Sequence 3, App1
25	178.8	2.9	48763	4 US-10-282-048-3	Sequence 3, App1
26	177.6	2.9	193	4 US-09-513-999C-20993	Sequence 20993, A
27	173	2.8	2188	4 US-09-949-016-2533	Sequence 2533, App

c	28	173	2.8	17455	4 US-09-949-016-14275	Sequence 14275, A
	29	172.2	2.8	4065	3 US-09-016-434-1105	Sequence 1105, App
	30	172.2	2.8	4739	3 US-08-685-871-1	Sequence 1, App1
	31	168.4	2.7	5053	2 US-08-685-576-2	Sequence 2, App1
	32	150.2	2.4	3323	2 US-08-422-699A-10	Sequence 10, App1
	33	150.2	2.4	3323	2 US-08-422-706B-10	Sequence 10, App1
	34	122.6	2.0	3155	3 US-09-442-100-7	Sequence 7, App1
	35	122.6	2.0	3155	4 US-08-939-106-7	Sequence 7, App1
	36	122.6	2.0	3155	4 US-09-442-102-7	Sequence 7, App1
	37	122.2	2.0	1998	3 US-09-509-902A-6	Sequence 6, App1
	38	122.2	2.0	1961	3 US-09-509-902A-15	Sequence 15, App1
	39	122.2	2.0	5276	2 US-09-233-857-2	Sequence 2, App1
	40	117.8	1.9	3018	2 US-08-860-150-6	Sequence 6, App1
	41	117.8	1.9	3018	3 US-09-338-132-6	Sequence 6, App1
	42	111.4	1.8	1935	2 US-08-878-989-11	Sequence 11, App1
	43	111.4	1.8	1935	3 US-09-272-795-11	Sequence 11, App1
	44	109.8	1.8	3213	3 US-09-442-100-5	Sequence 5, App1
	45	109.8	1.8	3213	4 US-08-939-106-5	Sequence 5, App1

ALIGNMENTS

480
32
1440

RESULT 1
US-10-028-946-1
Sequence 1, Application US/10028946
Patent No. 6734009
GENERAL INFORMATION:
APPLICANT: Yu, Xuanhuan
APPLICANT: Miranda, Maricar
APPLICANT: Fiddle, Carl Johan
TITLE OF INVENTION: No. 6734009 Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 60/258,335
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6165
TYPE: DNA
ORGANISM: homo sapiens
US-10-028-946-1

Query Match 91.9%; Score 5661.4; DB 4; Length 6165;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5944; Conservative 16; Indels 243; Gaps 3;

QY	1	ATGTTGAAGTTCAATATGAGCGCGGAATCTTTGATGCTGCTGTAACCCATT	60
DB	1	ATGTTGAAGTTCAATATGAGCGCGGAATCTTTGATGCTGCTGTAACCCATT	60
QY	61	GCCAGCGGGGCTCCAGGCTGAATCGTTCTCCAGGGGAAACCAACCTTTATGACTCA	120
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QY	121	CAGCAGATGTCCTCTCTTCCGAGAAAGATATGATGCTCTTTGTTCTTTGAA	180
DB	121	CAGCAGATGTCCTCTCTTCCGAGAAAGATATGATGCTCTTTGTTCTTTGAA	180
QY	181	GAATGATGCTGCTGCTCTGATGAATTAAGCACTGAGCAACTTTGTCGGAAGTAT	240
DB	181	GAATGATGCTGCTGCTCTGATGAATTAAGCACTGAGCAACTTTGTCGGAAGTAT	240
QY	241	TCCGACACCATATGCTGATTAAGAGCTCCAGCTTGCGGCAAGACTTGAAGTCA	300
DB	241	TCCGACACCATATGCTGATTAAGAGCTCCAGCTTGCGGCAAGACTTGAAGTCA	300
QY	301	ACTCTTGAAGTTGCTGCTCTGATGAGTGAAGTGAAGAGAAAGCAACCGGG	360
DB	301	ACTCTTGAAGTTGCTGCTCTGATGAGTGAAGTGAAGAGAAAGCAACCGGG	360

Qy	361	GACATCTATGCTATGAAAGTATGATAGAAAGAGCGCTTTATTTGGCCCGAGAGAGCTTTCA	420
Db	361	GACATCTATGCTATGAAAGTATGATAGAAAGAGCGCTTTATTTGGCCCGAGAGAGCTTTCA	420
Qy	421	TTTTTTGAGGAAGGCGGAACTATTTATCTCGAAGCAAGCCCGTGTGATCTCCCAATTA	480
Db	421	TTTTTTGAGGAAGGCGGAACTATTTATCTCGAAGCAAGCCCGTGTGATCTCCCAATTA	480
Qy	481	CAGTATGCTTTTCAAGCAAAAAATCACCTTTATCTGATGAGGAATTCAGCTGAGAGG	540
Db	481	CAGTATGCTTTTCAAGCAAAAAATCACCTTTATCTGATGAGGAATTCAGCTGAGAGG	540
Qy	541	GACTTGCTGCTACCTTTGAAATGATATGAGAGACAGATTTAATGAAAACCTGATATCAGTTT	600
Db	541	GACTTGCTGCTACCTTTGAAATGATATGAGAGACAGATTTAATGAAAACCTGATATCAGTTT	600
Qy	601	TACCTAGCTGAGCTGATTTTGGCTGTTCAAGCGTTTCATCTGATGGGATACGTGATCCGA	660
Db	601	TACCTAGCTGAGCTGATTTTGGCTGTTCAAGCGTTTCATCTGATGGGATACGTGATCCGA	660
Qy	661	GACATCAAGCTGAGAACTTCTCGTTGACCGCAAGAGACATCAAGCTGCTGATTTT	720
Db	661	GACATCAAGCTGAGAACTTCTCGTTGACCGCAAGAGACATCAAGCTGCTGATTTT	720
Qy	721	GGATCTGCCGCGAAAAATGAAATCAAAACAAGATGTAATGCAATGCCGATTTGGAGACC	780
Db	721	GGATCTGCCGCGAAAAATGAAATCAAAACAAGATGTAATGCAATGCCGATTTGGAGACC	780
Qy	781	CCAGATTAATAGGCTCTCTGAAGTCTGATCTGTGATGAACGGGGATGAAAAAGGCACTTAC	840
Db	781	CCAGATTAATAGGCTCTCTGAAGTCTGATCTGTGATGAACGGGGATGAAAAAGGCACTTAC	840
Qy	841	GGCCTGGACTGTGACTGTGTGTCAAGTGGCGGCTGATATGCTTATGATATGATTTATGGGAGA	900
Db	841	GGCCTGGACTGTGACTGTGTGTCAAGTGGCGGCTGATATGCTTATGATATGATTTATGGGAGA	900
Qy	901	TCCCCCTTGGCAGAGGGAACCTTCTGCCAAGACCTTCAATPAACATTATGAAATTTCCAGCGG	960
Db	901	TCCCCCTTGGCAGAGGGAACCTTCTGCCAAGACCTTCAATPAACATTATGAAATTTCCAGCGG	960
Qy	961	TTTTTGAATTTCCAGATGACCCCAAGAGAGACAGATCTTCTTGAATCTGATTCAAAGC	1020
Db	961	TTTTTGAATTTCCAGATGACCCCAAGAGAGACAGATCTTCTTGAATCTGATTCAAAGC	1020
Qy	1021	TTGTTGTGCGGCGCAGAAAGAGAGAGACTGAAAGTTTGAAGGCTCTTGTGCTGCCATCTTCTTC	1080
Db	1021	TTGTTGTGCGGCGCAGAAAGAGAGAGACTGAAAGTTTGAAGGCTCTTGTGCTGCCATCTTCTTC	1080
Qy	1081	TCATAAATTTGACTGGAACCAACTTGTGTAACCTCTCCCCCTTGTTGCCACCCCTCAAG	1140
Db	1081	TCATAAATTTGACTGGAACCAACTTGTGTAACCTCTCCCCCTTGTTGCCACCCCTCAAG	1140
Qy	1141	TCGACGATGACACTCCAAATTTTATGTAACCAAGAAAGAAATCGTGGGTTTCATCTCT	1200
Db	1141	TCGACGATGACACTCCCAATTTTATGTAACCAAGAAAGAAATCGTGGGTTTCATCTCT	1200
Qy	1201	CCGTCGACGCTGAGGCCCTCAGGCGCTTCTCGGTGTAAGAACTGCCGTTTGTGGGGTTTTTCG	1260
Db	1201	CCGTCGACGCTGAGGCCCTCAGGCGCTTCTCGGTGTAAGAACTGCCGTTTGTGGGGTTTTTCG	1260
Qy	1261	TACAGCAAGGCACTGGGGATTTCTTGATGATCTGAATCTGTTGTGTGTCGGGCTTGGAATCC	1320
Db	1261	TACAGCAAGGCACTGGGGATTTCTTGATGATCTGAATCTGTTGTGTGTCGGGCTTGGAATCC	1320
Qy	1321	CTCGCAAGACTAGCTTCATGGAAGAAAGAACTTCTCATCAAAAGCAAAAGACTTACAGAC	1380
Db	1321	CTCGCAAGACTAGCTTCATGGAAGAAAGAACTTCTCATCAAAAGCAAAAGACTTACAGAC	1380
Qy	1381	TCTCAGGCAAGTGTCACAAGATGAGAGAGAAATGATCCCGGTTTACATCGAGAGTGTCA	1440
Db	1381	TCTCAGGCAAGTGTCACAAGATGAGAGAGAAATGATCCCGGTTTACATCGAGAGTGTCA	1440
Qy	1441	GAGGTGGAAGGCTGTGCTTATGTCTCAGAGGAAGGTGAGACTGAAAGCCCTTGAACTTCAAGA	1500

[illegible]

Db 2521 CAAGAATGATGGCCCAAGAAGATGATTTCTGAATCTCAGGCAACAGAAATTTTAC 2580
Qy 2533 CTGAGACACAGGCTGGGAAGTTGGAGGCGCCAGAACCGAAACCTGAGAGAGAGAGCTGGAG 2592
Db 2581 CTGGAGACACAGGCTGGGAAGTTGGAGGCGCCAGAACCGAAACCTGAGAGAGAGAGCTGGAG 2640
Qy 2593 AAGATCAGACCAAGACCAAGTGAAGAAATCCGCTGCTGGAAGCTGGAGCAAGATTG 2652
Db 2641 AAGATCAGACCAAGACCAAGTGAAGAAATCCGCTGCTGGAAGCTGGAGCAAGATTG 2700
Qy 2653 CGGAGAGTCACTAGAGACAGAGAGAGAGAACTGAGCTCAAGGCCAGCTCAAGAG 2712
Db 2701 CGGAGAGTCACTAGAGACAGAGAGAGAGAACTGAGCTCAAGGCCAGCTCAAGAG 2760
Qy 2713 CTACAGCTCTCCCTGAGAGAGGCGGAGTCAAGTTGACAGCCCTGCAAGCTGCAAGGCG 2772
Db 2761 CTACAGCTCTCCCTGAGAGAGGCGGAGTCAAGTTGACAGCCCTGCAAGCTGCAAGGCG 2820
Qy 2773 GCGCTGGAGAGCAGCTTGGCCAGGCGAGAGACAGAGCTGGAAGAGACACAGAGAGCT 2832
Db 2821 GCGCTGGAGAGCAGCTTGGCCAGGCGAGAGACAGAGCTGGAAGAGACACAGAGAGCT 2880
Qy 2833 GAGAGAGATCCAGGCACTCAAGGCACTAAGAGTGAATCCAGCGCAATTTGATGCT 2892
Db 2881 GAGAGAGATCCAGGCACTCAAGGCACTAAGAGTGAATCCAGCGCAATTTGATGCT 2940
Qy 2893 CTTCGTAAACAGTGTACTGTAAATCAGACACTGGAGAGACAGCTAAACAGCTGACGAG 2952
Db 2941 CTTCGTAAACAGTGTACTGTAAATCAGACACTGGAGAGACAGCTAAACAGCTGACGAG 3000
Qy 2953 GAGAACGCTGAACCTCAACAAACCAAACTTCTACTGTCCAAACACTCGATAGAGCTTCT 3012
Db 3001 GAGAACGCTGAACCTCAACAAACCAAACTTCTACTGTCCAAACACTCGATAGAGCTTCT 3060
Qy 3013 GCGCGCAACGAGAGATTTGTAACACTGCGAAGTGAAGTGAACCATCTCCGCGGAGATC 3072
Db 3061 GCGCGCAACGAGAGATTTGTAACACTGCGAAGTGAAGTGAACCATCTCCGCGGAGATC 3120
Qy 3073 ACGGAACGAGAGATGAGCTTACACAGCCAGAAACCAACGATGAGGCTTTGAAGACACG 3132
Db 3121 ACGGAACGAGAGATGAGCTTACACAGCCAGAAACCAACGATGAGGCTTTGAAGACACG 3180
Qy 3133 TGCACCATGCTGAGAGAAAGAGTCAATGATTTGAGAGCCCTAAACGATGAGCTGAGAA 3192
Db 3181 TGCACCATGCTGAGAGAAAGAGTCAATGATTTGAGAGCCCTAAACGATGAGCTGAGAA 3240
Qy 3193 AAGAGACGAGTGGAGGCTGAGAGAGAGCTCTCGGAGTGAAGAAATCCAGTTTGAAG 3252
Db 3241 AAGAGACGAGTGGAGGCTGAGAGAGAGCTCTCGGAGTGAAGAAATCCAGTTTGAAG 3300
Qy 3253 TGTCCGGTTTGAAGCTGAGAGAAATGCTGAGACCCGAGAAACAGAGCAGGCGGAGAGCT 3312
Db 3301 TGTCCGGTTTGAAGCTGAGAGAAATGCTGAGACCCGAGAAACAGAGCAGGCGGAGAGCT 3360
Qy 3313 GATTCAGCGGATCAACCGAGTCTGCGCCAGGTGTGAGAGTGGAGTGAAGAGCAAGAGCT 3372
Db 3361 GATTCAGCGGATCAACCGAGTCTGCGCCAGGTGTGAGAGTGGAGTGAAGAGCAAGAGCT 3420
Qy 3373 GAGATTCTCGCTGAGAGAGGCTTCAAAAGAGCAAGAGTGAAGGCGGAGAGCTCTCT 3432
Db 3421 GAGATTCTCGCTGAGAGAGGCTTCAAAAGAGCAAGAGTGAAGGCGGAGAGCTCTCT 3480
Qy 3433 GACAACTCAATGACCTGAGAGAAAGATGCTATGCTTGAATGAAATGAAATGCCAGACTTA 3492
Db 3481 GACAACTCAATGACCTGAGAGAAAGATGCTATGCTTGAATGAAATGAAATGCCAGACTTA 3540
Qy 3493 CAGCGAAGCTGAGAGTGAAGAGAGCTCAACAGAGCTTCTGGAAGAGCAAGAGCAAA 3552
Db 3541 CAGCGAAGCTGAGAGTGAAGAGAGCTCAACAGAGCTTCTGGAAGAGCAAGAGCAAA 3600
Qy 3553 TTAACAGCAGAGTGAAGCTGAGAGAAATCAATTTTCCGTGTGACTCAAGAGCTGCA 3612
Db 3601 TTAACAGCAGAGTGAAGCTGAGAGAAATCAATTTTCCGTGTGACTCAAGAGCTGCA 3660

Qy 3613 GAAAGCTTAAGTCCGGCTGATCTACTGAAGACAGAAAGAAAGTGAAGCTTGGAGTACAGCTG 3672
Db 3661 GAAAGCTTAAGTCCGGCTGATCTACTGAAGACAGAAAGAAAGTGAAGTGAAGTACAGCTG 3720
Qy 3673 GAAAGCATTCAAGGTTCTCTAATCTCATGAAAGTGAAGTGAAGAGCACTATTTCTCA 3732
Db 3721 GAAAGCATTCAAGGTTCTCTAATCTCATGAAAGTGAAGTGAAGAGCACTATTTCTCA 3780
Qy 3733 CAACCAAACTCATTTGATTTTCTGCAAGCCAAATGACCAACCTGCTTAAAAAGAAAG 3792
Db 3781 CAACCAAACTCATTTGATTTTCTGCAAGCCAAATGACCAACCTGCTTAAAAAGAAAG -- 3838
Qy 3793 GGTTTATTTAGTCACGAGAAAGAGACCTCGCTTTAACCAACACAGGTTCTCTGAGTAC 3852
Db 3839 -----AGGTTCTCTGCAAGTAC 3855
Qy 3853 AATGAGCTGAAGCTGGCCCTGAGAGAGAGAAAGCTCGCTGTGACAGCTAAGAGAGCC 3912
Db 3856 AATGAGCTGAAGCTGGCCCTGAGAGAGAGAAAGCTCGCTGTGACAGCTAAGAGAGCC 3915
Qy 3913 CTTCAAGAGACCCGATGAGCTCCGCTCCGCGAGAGAAAGTGGCCCAACGCAAGCA 3972
Db 3916 CTTCAAGAGACCCGATGAGCTCCGCTCCGCGAGAGAAAGTGGCCCAACGCAAGCA 3975
Qy 3973 AAGGACCAACCCACACCAATCCACGCGCAGACACCGGAGAGACAGATGCGCATGTCGCC 4032
Db 3976 AAGGACCAACCCACACCAATCCACGCGCAGACACCGGAGAGACAGATGCGCATGTCGCC 4035
Qy 4033 ATCGTCCGGTCCGACAGAGACCAAGCCAGTGCATGAGCTGTGAGCCCGGCAATCCAGC 4092
Db 4036 ATCGTCCGGTCCGACAGAGACCAAGCCAGTGCATGAGCTGTGAGCCCGGCAATCCAGC 4095
Qy 4093 CGCAGAAAGAGTCTTCAACTTCAAGAGAAATTTAGTCCGCTTTAAGAAACGATGCAAC 4152
Db 4096 CGCAGAAAGAGTCTTCAACTTCAAGAGAAATTTAGTCCGCTTTAAGAAACGATGCAAC 4155
Qy 4153 CACATATTTCTCAACCGATTTCAACCTTAGAGCTGAACATGCGAGCCACAAAGTGTCTGAG 4212
Db 4156 CACATATTTCTCAACCGATTTCAACCTTAGAGCTGAACATGCGAGCCACAAAGTGTCTGAG 4215
Qy 4213 TGTCTGATACCGTGCATTTGAGAGCCAGGATCCAAATGTCTGAAATGTGAGGTGATG 4272
Db 4216 TGTCTGATACCGTGCATTTGAGAGCCAGGATCCAAATGTCTGAAATGTGAGGTGATG 4275
Qy 4273 TGTCAACCCCAAGTGTCCACGCTTGTGCCAGCCCTGCGGCTTGTGTAATATGCC 4332
Db 4276 TGTCAACCCCAAGTGTCCACGCTTGTGCCAGCCCTGCGGCTTGTGTAATATGCC 4335
Qy 4333 ACACATTTCAACGAGAGGCTTGTGCCGTGACAAATGAACTCCCAAGGTCTCCAGACCAAG 4392
Db 4336 ACACATTTCAACGAGAGGCTTGTGCCGTGACAAATGAACTCCCAAGGTCTCCAGACCAAG 4395
Qy 4393 GAGCCAGCAGAGCTTGCACCTGGAAGGAGTGAAGGTGCCAGAAATTAACAAACGA 4452
Db 4396 GAGCCAGCAGAGCTTGCACCTGGAAGGAGTGAAGGTGCCAGAAATTAACAAACGA 4455
Qy 4453 GGAACAGCAAGGCTGGAGACAGAAATGATCTGTCTGAGAGATCAAAAGTCTCATTAAT 4512
Db 4456 GGAACAGCAAGGCTGGAGACAGAAATGATCTGTCTGAGAGATCAAAAGTCTCATTAAT 4515
Qy 4513 GACATTAAGAACCAAGAAAGTGGACAGAGAGCCGGGTGGAAGAAATTTGAGCTGTGCCCTCC 4572
Db 4516 GACATTAAGAACCAAGAAAGTGGACAGAGAGCCGGGTGGAAGAAATTTGAGCTGTGCCCTCC 4575
Qy 4573 GACGGGAGTGTATTAATTCATGAGTCCGCTGTGCTCCGAATCTGCAAAATACAGCCAAA 4632
Db 4576 GACGGGAGTGTATTAATTCATGAGTCCGCTGTGCTCCGAATCTGCAAAATACAGCCAAA 4635
Qy 4633 GCA----- 4635
Db 4636 GCAGATGTCCCATATACATACTGAAGATGAAATCTCACCCGACACACACCTGTGCGCCGGG 4695

[illegible]

Db	5776	AAGGAAAACCTCGTGAAGAGTCCGGACATGAAACACACCGGGGCCGTCCACTCCGC	5835
OY	5683	AGCAGCCCAACAAGCAGAGGCCACCCACGTACACAGACATCAACCAAGCGGTGAC	5742
Db	5896	AGAGCCCTCAACAAGCCAGGCGCCACCCACGTACAAACAGCACAATCAACAAGCGGTGGC	5895
OY	5743	TCGAGCCCAAGCGCGCCCGCAAGAGCCCAAGCCCAACCGGAGAGCCCAAGCACCACCGC	5802
Db	5896	TCGAGCCCAAGCGCGCCCGCAAGAGCCCAAGCCCAAGCCCAAGCACCACCGC	5955
OY	5803	TACCGCAGGAGGCGCGACCGAGCTCGCAGAGGACAAGTCTCTTGCGCCGCCCTTGAGCGA	5862
Db	5956	TACCGCAGGAGGCGCGACCGAGCTCGCAGAGGACAAGTCTCTTGCGCCGCCCTTGAGCGA	6015
OY	5863	GAGAAATCCCCCGGCGCGAATGCTCAGCACCGCGAGAGAGCGGTCCCGCGGAGGCTGTTT	5922
Db	6016	GAGAAATCCCCCGGCGCGAATGCTCAGCACCGCGAGAGAGCGGTCCCGCGGAGGCTGTTT	6075
OY	5923	GAAGACAGCAGCAGAGGCGCGGCTGCTGCGGAGACCGTGAGGACCCCGCTGTCCAGATG	5982
Db	6076	GAAGACAGCAGCAGAGGCGCGGCTGCTGCGGAGACCGTGAGGACCCCGCTGTCCAGATG	6135
OY	5983	AACAAGGAAAGGCGCAGAGTGC	6005
Db	6136	AACAAGGCTGGGACCAAGTCTTC	6158

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RESULT 2
US-10-028-946-3
/ Sequence 3, Application US/10028946
/ Patent No. 6734009
/ GENERAL INFORMATION:
/ APPLICANT: Yu, Xuanchuan
/ APPLICANT: Miranda, Maricar
/ APPLICANT: Fiddie, Carl Johan
/ TITLE OR INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same
/ FILE REFERENCE: LEX-0289-USA
/ CURRENT APPLICATION NUMBER: US/10/028,946
/ CURRENT FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: US 60/258,335
/ PRIOR FILING DATE: 2000-12-27
/ NUMBER OF SEQ. ID NOS: 4
/ SOFTWARE: PaateSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 5877
/ TYPE: DNA
/ ORGANISM: homo sapiens
US-10-028-946-3

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Query Match	87.0%	Score 5358	DB 4	Length 5877
Best Local Similarity	95.8%	Pred. No. 0		
Matches 5634	Conservative	0	Mismatches 5	Indels 243
			Gaps	3
QY	1	ATGTTGAAGTTCAAAATATGAGGCGCGGAATCCTTTGATGCTGCTGTAACCCATT	60	
Db	1	ATGTTGAAGTTCAAAATATGAGGCGCGGAATCCTTTGATGCTGCTGTAACCCATT	60	
QY	61	GCCAGCGCGGCGCTCCAGGCTGAATCTGTTTCCAGGGGAACACCCCTTATGACTCAA	120	
Db	61	GCCAGCGGCGCTCCAGGCTGAATCTGTTTCCAGGGGAACACCCCTTATGACTCAA	120	
QY	121	CAGCAGATGTCCTCTCTTTTCCGAGAAAGGATATTAGATGCCCTCTTGTCTCTTTGAA	180	
Db	121	CAGCAGATGTCCTCTCTTTTCCGAGAAAGGATATTAGATGCCCTCTTGTCTCTTTGAA	180	
QY	181	GAAATGAGTAGGCTGCTCGATGAAGAATTAAACACATGAGCAACTTTGCGCGGAAGTAT	240	
Db	181	GAAATGAGTAGGCTGCTCGATGAAGAATTAAACACATGAGCAACTTTGCGCGGAAGTAT	240	
QY	241	TCCGACACCAATAGCTGATTAACAGAGCTTCAGACTTTGGCCAAAGGACTTGAAGTCAG	300	
Db	241	TCCGACACCAATAGCTGATTAACAGAGCTTCAGACTTTGGCCAAAGGACTTGAAGTCAG	300	

OY	301	AGCTGTAAGGTGGTCACTTTGCTGAAGCAGGGGTAAAGAGAAAGCAACGGG	360
Db	301	AGCTTGTAGGTGGTCACTTTGCTGAAGTGAAGGTGAAGAGAAAGCAACGGG	360
OY	361	GACATCTATGCTATGAAAGTGAAGAGAGGCTTTATTGGCCACAGACAGGTTCA	420
Db	361	GACATCTATGCTATGAAAGTGAAGAGAGGCTTTATTGGCCACAGACAGGTTCA	420
OY	421	TTTTTTGAGAAAGCGGACATATTACTGAAACACAGCCGTGATCCCCAATTA	480
Db	421	TTTTTTGAGAAAGCGGACATATTACTGAAACACAGCCGTGATCCCCAATTA	480
OY	481	CAGATGACCTTTCAGAGCAAAAATACCTTTATCTGAAGGAAATCAGCCTGAGGG	540
Db	481	CAGATGACCTTTCAGAGCAAAAATACCTTTATCTGAAGGAAATCAGCCTGAGGG	540
OY	541	GAATTTGCTGCACTTTGAAATGATGAGGACAGTTAGTAAACCTGATACATTT	600
Db	541	GACTTGCTGCACTTTGAAATGATGAGGACAGTTAGTAAACCTGATACATTT	600
OY	601	TACCTAGCTGAGCTGATTTTGGCTGTCAAGCTTCACTGATGGATAGCTGATGA	660
Db	601	TACCTAGCTGAGCTGATTTTGGCTGTCAAGCTTCACTGATGGATAGCTGATGA	660
OY	661	GAGATCAAGCCTGAGAACATTTCTGTTACCGCACAGACACATCAAGCTGTGATTT	720
Db	661	GAGATCAAGCCTGAGAACATTTCTGTTACCGCACAGACACATCAAGCTGTGATTT	720
OY	721	GGAATGTCGGCGGAAATGATTTCAACCAAGATGTGAATGCCAATCTCCGATTTGG	780
Db	721	GGAATGTCGGCGGAAATGATTTCAACCAAGATGTGAATGCCAATCTCCGATTTGG	780
OY	781	CCAGATTCATAGGCTCTGTAAGTGTGACTGTGATGAACGGGGATGAAAAAGCACCTAC	840
Db	781	CCAGATTCATAGGCTCTGTAAGTGTGACTGTGATGAACGGGGATGAAAAAGCACCTAC	840
OY	841	GAGCTGGAAGCTGAGCTGGTGGTCAAGTGGGCGTATGCTATGAGATGATTTATGGAGA	900
Db	841	GAGCTGGAAGCTGAGCTGGTGGTCAAGTGGGCGTATGCTATGAGATGATTTATGGAGA	900
OY	901	TCCCCCTTCGAGAGGGAACTCTGCGCCAAACCTCAATAACATTATGAAATTTCAAGGG	960
Db	901	TCCCCCTTCGAGAGGGAACTCTGCGCCAAACCTCAATAACATTATGAAATTTCAAGGG	960
OY	961	TTTTTGAATTTCCAGATGACCCCAATGAGCACTGACTTTCTTGATCTGAATTCAAAGC	1020
Db	961	TTTTTGAATTTCCAGATGACCCCAATGAGCACTGACTTTCTTGATCTGAATTCAAAGC	1020
OY	1021	TTGTTTGTGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGTGCTATCTTTCTTC	1080
Db	1021	TTGTTTGTGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGTGCTATCTTTCTTC	1080
OY	1081	TCTAAAAATTGACTGGACAACTTCGTAACTCTCTCCCTCCCTGTTCCACCTCAAG	1140
Db	1081	TCTAAAAATTGACTGGACAACTTCGTAACTCTCTCCCTCCCTGTTCCACCTCAAG	1140
OY	1141	TCTGACGATGACACCTCCAAATTTTGATGAAACGAGAGAAATCGTGGGTTCACTCTC	1200
Db	1141	TCTGACGATGACACCTCCAAATTTTGATGAAACGAGAGAAATCGTGGGTTCACTCTC	1200
OY	1201	CCGTGACCAAGTGAAGCCCTCAAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTCG	1260
Db	1201	CCGTGACCAAGTGAAGCCCTCAAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTCG	1260
OY	1261	TACAGCAAGCACTGGGATTTCTTGGTGAATCTGATGCTGTGTGTCGGGCTGGAACCTC	1320
Db	1261	TACAGCAAGCACTGGGATTTCTTGGTGAATCTGATGCTGTGTGTCGGGCTGGAACCTC	1320
OY	1321	CTGTGCAAGACTAGCTCCATGGAAGAACTTCTCATCAAGCAAGAGCTACAGAC	1380
Db	1321	CTGTGCAAGACTAGCTCCATGGAAGAACTTCTCATCAAGCAAGAGCTACAGAC	1380

OY	1381	CTCAGAGCAAGTGTCTCAGATGAGAGGAAATGACCCGGTTACATCGGAGGTGCA	1448
Db	1381	TCTCAGAGCAAGTGTCTCAGATGAGAGGAAATGACCCGGTTACATCGGAGGTGCA	1440
OY	1441	GAGGTGAGGCTGTGCTTACTCAGAGGAGGTGAGGCTGAAAGGCTCTGAGACTCAGAGA	1500
Db	1441	GAGGTGAGGCTGTGCTTACTCAGAGGAGGTGAGGCTGAAAGGCTCTGAGACTCAGAGA	1500
OY	1501	TCCTCTCTGAGCAGAGCTTTGCTACCTACATCAGAAATGCACTAGCTTAAACGAAAGT	1560
Db	1501	TCCTCTCTGAGCAGAGCTTTGCTACCTACATCAGAAATGCACTAGCTTAAACGAAAGT	1560
OY	1561	TTGAGAGCAGACCGGATGAGAGGTGTCCCGAGAGATGCAAAAGCATGCACTTCTCAT	1620
Db	1561	TTGAGAGCAGACCGGATGAGAGGTGTCCCGAGAGATGCAAAAGCATGCACTTCTCAT	1620
OY	1621	GATATCAGAGAGCAGAGCCGAGACTCCAGAAATCAAAGAGCAGAGTACAGAGCTCAA	1680
Db	1621	GATATCAGAGAGCAGAGCCGAGACTCCAGAAATCAAAGAGCAGAGTACAGAGCTCAA	1680
OY	1681	GTGGAAGAAATGAGGTTGATGATGAATCAGTTGGAAAGGATCTTGTCTCAGCAAGAGA	1740
Db	1681	GTGGAAGAAATGAGGTTGATGATGAATCAGTTGGAAAGGATCTTGTCTCAGCAAGAGA	1740
OY	1741	CGGAGTGTCTCTACGAATCTGAGCTGAGAGATCTCGGCTTGCTGCTGAAGAAATTCAG	1800
Db	1741	CGGAGTGTCTCTCTACGAATCTGAGCTGAGAGATCTCGGCTTGCTGCTGAAGAAATTCAG	1800
OY	1801	CGGAAAGGGAAGAAATGTCAAGCATTAATCTGTTGAAGGCTAAGATCAAAGGAGACTGAA	1860
Db	1801	CGGAAAGGGAAGAAATGTCAAGCATTAATCTGTTGAAGGCTAAGATCAAAGGAGACTGAA	1860
OY	1861	GTGGGAGAAATGCGGAACTGAGAGAGTCAATGCTGAGCAGCAGCTCAAAATTCAGAG	1920
Db	1861	GTGGGAGAAATGCGGAACTGAGAGAGTCAATGCTGAGCAGCAGCTCAAAATTCAGAG	1920
OY	1921	CTCCAGAGAAATCTGAGAGGCT-----1944	
Db	1921	CTCCAGAGAAATCTGAGAGAGGCTGTAAAAAGCCAGCACGAGGCCACGAGCTGTCAG	1980
OY	1945	-----GAAAGAGGCGAGCCGAGAGGAGGAGCTGAGAGCTGCAAGCCGAGAG	1992
Db	1981	AATATCCGCGCAGGCAAGAGAGCCGAGAGGAGCTGAGAGCTGCAAGCCGAGAG	2040
OY	1993	GATTCCTCTGAGAGCATCAGAAAGAACTGGTGAACCTGAGGAAACGCCGCAATTCCTG	2052
Db	2041	GATTCCTCTGAGAGCATCAGAAAGAACTGGTGAACCTGAGGAAACGCCGCAATTCCTG	2100
OY	2053	GAGAACAAAGTTAAAGAGCTAGAGACCATGAGCGGTAGAGAAAAGCATGTAAGGATGAC	2112
Db	2101	GAGAACAAAGTTAAAGAGCTAGAGACCATGAGCGGTAGAGAAAAGCATGTAAGGATGAC	2160
OY	2113	ATCCAGACAAAAATCCCAACAGATCCAGCAGATGGCTGATAAATTTCTGAGCTTGAAAG	2172
Db	2161	ATCCAGACAAAAATCCCAACAGATCCAGCAGATGGCTGATAAATTTCTGAGCTTGAAAG	2220
OY	2173	AAACATCGGAGGCGCCAGTCTCAGCCCAGACCTAGAAAGTGCACCTGAAACAGAAAGAG	2232
Db	2221	AAACATCGGAGGCGCCAGTCTCAGCCCAGACCTAGAAAGTGCACCTGAAACAGAAAGAG	2280
OY	2233	CAGCACTATGAGAAAAAGTTAAAGTGTGAGCAATCAGATTAAGAAAGACTTGCTGAC	2292
Db	2281	CAGCACTATGAGAAAAAGTTAAAGTGTGAGCAATCAGATTAAGAAAGACTTGCTGAC	2340
OY	2293	AAGAGACACTGAGAAACATGATCAGAGACAGAGAGAGGCTCATGAGAGGCAAA	2352
Db	2341	AAGAGACACTGAGAAACATGATCAGAGACAGAGAGAGGCTCATGAGAGGCAAA	2400
OY	2353	ATTCTCAGCGCAAGAAAGGCGATGATCAAGCTATGGAATTCAGAGTCAAGTCCCTGAAA	2412
Db	2401	ATTCTCAGCGCAAGAAAGGCGATGATCAAGCTATGGAATTCAGAGTCAAGTCCCTGAAA	2460
OY	2413	CAGGAGATGTGAACTGTCTGAAGCCAAATAAATTGCAAGCAATAGACTTTTAAAC	2472

Db	2461	CAGAGGATGTGGAACTGTCTGGAAGCCATTAACCTTTCAGCAATTAACAGTCTTTTACC	2520
Qy	2473	CAAGGAACATGAAGGCCCAAGAAAGATGATTTCTGAACCTCAGGCAACAGAAATTTTAC	2532
Db	2521	CAAGGAACATGAAGGCCCAAGAAAGATGATTTCTGAACCTCAGGCAACAGAAATTTTAC	2580
Qy	2533	CTGGAGACACAGGCTGGGAAGTTGGAGGCCGAGAACCGAAACCTGGAGAGCAGCTGGAG	2592
Db	2581	CTGGAGACACAGGCTGGGAAGTTGGAGGCCGAGAACCGAAACCTGGAGAGCAGCTGGAG	2640
Qy	2593	AAGATCAGCCACCAAGACCAACAGTGAACAAGATCGCTCTGGAACTGGAGACAAGATTG	2652
Db	2641	AAGATCAGCCACCAAGACCAACAGTGAACAAGATCGCTCTGGAACTGGAGACAAGATTG	2700
Qy	2653	CGGAGGTCAGTCTAGAGGACGAGAGACAGAAATCTGAAGCTCAAGGCCAGCTCACAGAG	2712
Db	2701	CGGAGGTCAGTCTAGAGGACGAGAGACAGAAATCTGAAGCTCAAGGCCAGCTCACAGAG	2760
Qy	2713	CTACAGCTCTCCCTGCAAGAGCGGAGTCAAGCTTGAACAGCTCTGACGGCTGACGGGGG	2772
Db	2761	CTACAGCTCTCCCTGCAAGAGCGGAGTCAAGCTTGAACAGCTCTGACGGCTGACGGGGG	2820
Qy	2773	GCCCTGGAAGCCAGCTTCCGCGAGGCGAAGACAGAGCTGGAAAGACCAACAGCAAGAGCT	2832
Db	2821	GCCCTGGAAGCCAGCTTCCGCGAGGCGAAGACAGAGCTGGAAAGACCAACAGCAAGAGCT	2880
Qy	2833	GAAGAGAGATCCAGGCACTCAGGGAACATAGAGATGAATCCAGGCGCAATTTGATGCT	2892
Db	2881	GAAGAGAGATCCAGGCACTCAGGGAACATAGAGATGAATCCAGGCGCAATTTGATGCT	2940
Qy	2893	CTTCGTAAACAGCTGTACTGTAAATCAGACCTGGAGAGACAGCTAAACAGCTGACCGAG	2952
Db	2941	CTTCGTAAACAGCTGTACTGTAAATCAGACCTGGAGAGACAGCTAAACAGCTGACCGAG	3000
Qy	2953	GAACAAGCTGAAGTCAACCAACAACTTCTACTTTCCTCAAACTCATGATGAGCTTCT	3012
Db	3001	GAACAAGCTGAAGTCAACCAACAACTTCTACTTTCCTCAAACTCATGATGAGCTTCT	3060
Qy	3013	GGCGCCAAACGAGAGATTGTAACTGCGAAGTGAAGTGAACCATCTCCGCGGAGATGTC	3072
Db	3061	GGCGCCAAACGAGAGATTGTAACTGCGAAGTGAAGTGAACCATCTCCGCGGAGATGTC	3120
Qy	3073	AAGGAACGAGATGCAAGCTTACCGACCAAGAACCAACGATGAGGCTCTGAAGACCAAG	3132
Db	3121	AAGGAACGAGATGCAAGCTTACCGACCAAGAACCAACGATGAGGCTCTGAAGACCAAG	3180
Qy	3133	TGCACCATGCTGAGAGAACAGGTCAATGATTGGAGGCCCTTAACGATGAGCTGCTAAGA	3192
Db	3181	TGCACCATGCTGAGAGAACAGGTCAATGATTGGAGGCCCTTAACGATGAGCTGCTAAGA	3240
Qy	3193	AAAGACCGGCAATGGGAGGCCCTGAGAGAGCGTCTGGGTGATGAGAAATCCAGTTTGAAG	3252
Db	3241	AAAGACCGGCAATGGGAGGCCCTGAGAGAGCGTCTGGGTGATGAGAAATCCAGTTTGAAG	3300
Qy	3253	TGTGGGGTTCCGAGAGCTGAGAGAAATGCTGGAACACCGAGAAACAGAGCCGAGAGCC	3312
Db	3301	TGTGGGGTTCCGAGAGCTGAGAGAAATGCTGGAACACCGAGAAACAGAGCCGAGAGCC	3360
Qy	3313	GATCAGCGGATCACCGAGTCTCGCCAGGTGGTGAAGCTGGCAGTGAAGAGACCAAGGCT	3372
Db	3361	GATCAGCGGATCACCGAGTCTCGCCAGGTGGTGAAGCTGGCAGTGAAGAGACCAAGGCT	3420
Qy	3373	GAGATTCTCGCTCTGCAAGAGGCTTCAAGAGCAAGAGCTGAAGCCGAGAGGCTCTCT	3432
Db	3421	GAGATTCTCGCTCTGCAAGAGGCTTCAAGAGCAAGAGCTGAAGCCGAGAGGCTCTCT	3480
Qy	3433	GACAAGCTCAATGAAGCTGGAAGAGAGATGCTTGAAGAAATGATGCCGAAGCTTGA	3492
Db	3481	GACAAGCTCAATGAAGCTGGAAGAGAGATGCTTGAAGAAATGATGCCGAAGCTTGA	3540
Qy	3493	CAGCAAGGCTGGAAGCTGAAGCAGAGGCTCAACAGAGGCTTCTGAAGAGCAAGCCAA	3552
Db	3541	CAGCAAGGCTGGAAGCTGAAGCAGAGGCTCAACAGAGGCTTCTGAAGAGCAAGCCAA	3600
Qy	3553	TTACAGCAGCAGATGGAAGCTGCAAGAAAATGACATTTTCCGCTTACATCAAGAGATGCA	3612
Db	3601	TTACAGCAGCAGATGGAAGCTGCAAGAAAATGACATTTTCCGCTTACATCAAGAGATGCA	3660
Qy	3613	GAAAGCTTAAGATCGGCTGATCTACTGAAGACAGAAAGAGTCACTTGAAGATCAGCTG	3672
Db	3661	GAAAGCTTAAGATCGGCTGATCTACTGAAGACAGAAAGAGTCACTTGAAGATCAGCTG	3720
Qy	3673	GAAAACATTCAGGTTCTCTAATCTCAATGAAGAAAGTGAAGAAAGGACATATTTCTCA	3732
Db	3721	GAAAACATTCAGGTTCTCTAATCTCAATGAAGAAAGTGAAGAAAGGACATATTTCTCA	3780
Qy	3733	CAAAACCAATCTCATTTGATTTTCTGCAAGCCAAAATGACCAACCTGCTAAAAAGAAAAG	3792
Db	3781	CAAAACCAATCTCATTTGATTTTCTGCAAGCCAAAATGACCAACCTGCTAAAAAGAAAAG	3840
Qy	3793	GGTTTATTTAGTCCAGGAGAAAGAGACCTGCTTTAACCAACAGGTTCTCTGCAATAC	3852
Db	3839	-----AGTTCTCTGCAATAC-----	3855
Qy	3853	AATGAGCTGAAGCTGGCCCTGGAAGAGAGAAAGCTGCTGTGCAAGCTAGAGAAAGCC	3912
Db	3856	AATGAGCTGAAGCTGGCCCTGGAAGAGAGAAAGCTGCTGTGCAAGCTAGAGAAAGCC	3915
Qy	3913	CTTCAGAAAGACCCGCAATGAGCTCCGCTCCGCGCGGAGAGAAAGTGGCCACCGCAAGCA	3972
Db	3916	CTTCAGAAAGACCCGCAATGAGCTCCGCTCCGCGCGGAGAGAAAGTGGCCACCGCAAGCA	3975
Qy	3973	AAGGACCAACCAACCCATCCAGCCGACCCGCGAGGAGAGAGTGGCCACCGCAATGTC	4032
Db	3976	AAGGACCAACCAACCCATCCAGCCGACCCGCGAGGAGAGAGTGGCCACCGCAATGTC	4035
Qy	4033	ATCGTGCAGTCCGCAAGAGCAACAGCCAGTGCATGAGCTGTGCGGCCCGCCATCCAGC	4092
Db	4036	ATCGTGCAGTCCGCAAGAGCAACAGCCAGTGCATGAGCTGTGCGGCCCGCCATCCAGC	4095
Qy	4093	CGCAGAAAGAGTCTTCAATCCAGAGAAATTTAGTGGCGTCTTAAAGAACCATGAC	4152
Db	4096	CGCAGAAAGAGTCTTCAATCCAGAGAAATTTAGTGGCGTCTTAAAGAACCATGAC	4155
Qy	4153	CACAATATTCCTCAACCGATTCACGTAAGCAATGAGACCAACAAAGTGTGCTG	4212
Db	4156	CACAATATTCCTCAACCGATTCACGTAAGCAATGAGACCAACAAAGTGTGCTG	4215
Qy	4213	TGTCGTGAATCCGTGCACTTTGGAACGCAAGCATCCAAATGTCTGCAATGTCAAGTATG	4272
Db	4216	TGTCGTGAATCCGTGCACTTTGGAACGCAAGCATCCAAATGTCTGCAATGTCAAGTATG	4275
Qy	4273	TGTCACCCCAAGTGTCCACATGCTTGGCCAGCCACTGGGCTTGGCTGTGAATATGCC	4332
Db	4276	TGTCACCCCAAGTGTCCACATGCTTGGCCAGCCACTGGGCTTGGCTGTGAATATGCC	4335
Qy	4333	ACAACATTCACCGAGGCTTCTGCGTGAACAAATGAACCTCCCAAGTCTCCAGCAAG	4392
Db	4336	ACAACATTCACCGAGGCTTCTGCGTGAACAAATGAACCTCCCAAGTCTCCAGCAAG	4395
Qy	4393	GAGCCCAAGCAGGCTTGGCACTGGAAGGAGTGAAGAGTGTCCAGAAATACAAACGA	4452
Db	4396	GAGCCCAAGCAGGCTTGGCACTGGAAGGAGTGAAGAGTGTCCAGAAATACAAACGA	4455
Qy	4453	GGAACAGAGGCTGGGAGACGAAATGATTTGTCTGGAAGGATCAAAATCTCTCATTTAT	4512
Db	4456	GGAACAGAGGCTGGGAGACGAAATGATTTGTCTGGAAGGATCAAAATCTCTCATTTAT	4515
Qy	4513	GACATGAAGCCAGAGAGCTGGAACAGAGCCGAGTGAAGAAATTTGAGCTGTGCTTCC	4572
Db	4516	GACATGAAGCCAGAGAGCTGGAACAGAGCCGAGTGAAGAAATTTGAGCTGTGCTTCC	4575
Qy	4573	GACGGGAGATGATCTATTTATGAGTGCCTTGGTGTCTCCGAACCTGCAAAATACAGCCAA	4632
Db	4576	GACGGGAGATGATCTATTTATGAGTGCCTTGGTGTCTCCGAACCTGCAAAATACAGCCAA	4635

4633 GCA----- 4635
4636 GGAAGATGCCATACATCTGAAAGATGAACTCACCCGACACACCTGCGCCGCG 4695
4636 ----- 4635
4696 AAGACCTCTACTTGTAGTCTCCAGCTTCCCTGACAAAACAGCGCTGGGTCAACCGCTTA 4755
4636 ----- 4662
4756 GAATCATTTGTGCAAGTGGAGAGATTCTTACGGAAAAAGACAGAACTGATGCTAAACTG 4815
4663 CTGGAAAACTCCCTGCTGTAACCTGGAAGTGAACCTGCTTAACAATGAACTGCAAGCTG 4722
4816 CTGGAAATCTCCCTGCTGTAACCTGGAAGTGAACCTGCTTAACAATGAACTGCAAGCTG 4875
4723 CCCTTCAGTGAACAGGTGCTGTTGTTGAGGCAACGAGAAAGGCTCTACGCTCTGAATGTC 4782
4876 CCCTTCAGTGAACAGGTGCTGTTGTTGAGGCAACGAGAAAGGCTCTACGCTCTGAATGTC 4935
4783 TTGAAAACTCCCTTAACCAATGTCACAGAAATTTGAGAGCTTCCAAATTTATATTATC 4842
4936 TTGAAAACTCCCTTAACCAATGTCACAGAAATTTGAGAGCTTCCAAATTTATATTATC 4995
4843 AAGGACCTGGAAGAGTACTCTGATGATGAGAGAGAAAGAGGAGTCTGCTTGTGAGC 4902
4996 AAGGACCTGGAAGAGTACTCTGATGATGAGAGAGAAAGAGGAGTCTGCTTGTGAGC 5055
4903 GTGAAAGAAAGTGAACAGTCCCTGAGCCAGTCCCACTGCTGCTCCAGCCGACATCTCA 4962
5056 GTGAAAGAAAGTGAACAGTCCCTGAGCCAGTCCCACTGCTGCTCCAGCCGACATCTCA 5115
4963 CCCAACTTTTGAAGCTGTCAAGAGGCTGCAACTTGTGAGGAGAGGAGAAATTTGAGAA 5022
5116 CCCAACTTTTGAAGCTGTCAAGAGGCTGCAACTTGTGAGGAGAGGAGAAATTTGAGAA 5175
5023 GGGCTTGTGATCTGTGCAAGCCATGCGCCAGCAAGTGTGATCTTCCGCTCAACAGAAAC 5082
5176 GGGCTTGTGATCTGTGCAAGCCATGCGCCAGCAAGTGTGATCTTCCGCTCAACAGAAAC 5235
5083 CTGAGCAATTAATCTGATCCGAGAAAGAGATGAGAGCTCAGAGGCTGAGCTGTATCCAC 5142
5236 CTGAGCAATTAATCTGATCCGAGAAAGAGATGAGAGCTCAGAGGCTGAGCTGTATCCAC 5295
5143 TTACCAATTAATCTGATCTGATGAGCAATTAATTTTACGAAATTCGACATGAGCAAG 5202
5296 TTACCAATTAATCTGATCTGATGAGCAATTAATTTTACGAAATTCGACATGAGCAAG 5355
5203 TACAGCTGTGAGGAATTTCTGATGATGAGCAATTTCTGAGCACTGCTGTGTTGCC 5262
5356 TACAGCTGTGAGGAATTTCTGATGATGAGCAATTTCTGAGCACTGCTGTGTTGCC 5415
5263 GCGCTTTCAACAGCTTCCCTGCTCAATGCTGAGAGTGAACAGGAGGAGGAGAG 5322
5416 GCGCTTTCAACAGCTTCCCTGCTCAATGCTGAGAGTGAACAGGAGGAGGAGAG 5475
5323 GAGTACTTGTGCTGTTTCCAGCAATTTGAGTGTGCTGATTTTACGGAAGAGCTGAGC 5382
5476 GAGTACTTGTGCTGTTTCCAGCAATTTGAGTGTGCTGATTTTACGGAAGAGCTGAGC 5535
5383 CGGACAGAGATTTCAAGTGAAGTCCCTTAACCTTTGAGCTTTGCTCAAGAAACCTTAT 5442
5536 CGGACAGAGATTTCAAGTGAAGTCCCTTAACCTTTGAGCTTTGCTCAAGAAACCTTAT 5595
5443 CTGTTGTGACCACTTCAACTCACTGAAATGTAATTGAGATCCAGGCAAGCTCTCTGAGCA 5502
5596 CTGTTGTGACCACTTCAACTCACTGAAATGTAATTGAGATCCAGGCAAGCTCTCTGAGCA 5655
5503 GGGAGCCCTGAGCCGAGAGCTGAGCAATCCGAAACCGGCTTACCTGAGGCTCTGCCATT 5562
5656 GGGAGCCCTGAGCCGAGAGCTGAGCAATCCGAAACCGGCTTACCTGAGGCTCTGCCATT 5715

QY 5563 TCCTCAGAGCGATTACTTGGCGTCTCATACAGATTAATTAAGGCTCATTTGCTGC 5622
DB 5716 TCCTCAGAGCGATTACTTGGCGTCTCATACAGATTAATTAAGGCTCATTTGCTGC 5775
QY 5623 AAGGAAACCTGCTGAGAGAGTCCGCACTGAACCAACCGGAGGCTGCTCACTCCGC 5682
DB 5776 AAGGAAACCTGCTGAGAGAGTCCGCACTGAACCAACCGGAGGCTGCTCACTCCGC 5835
QY 5683 AG 5684
DB 5836 AG 5837

RESULT 3

US-09-804-471A-1
; Sequence 1, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Human
US-09-804-471A-1

Query Match 22.6%; Score 1391.8; DB 4; Length 1515;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1396; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGTGAATTTCAATATGAGAGCGGGAATCCCTTGGAGTGTGCTGCTGAACCAATT 60
DB 7 ATGTGAATTTCAATATGAGAGCGGGAATCCCTTGGAGTGTGCTGCTGAACCAATT 66
QY 61 GCCAGCCGGGCTCCAGGCTGATCTGTTCTTCAAGGAGAAACCACTTTATGACTCAA 120
DB 67 GCCAGCCGGGCTCCAGGCTGATCTGTTCTTCAAGGAGAAACCACTTTATGACTCAA 126
QY 121 CAGCAGATGTCTCTTTTCCGAGAGGAGATTTAGATCCCTCTTTGTTCTTTGAA 180
DB 127 CAGCAGATGTCTCTTTTCCGAGAGGAGATTTAGATCCCTCTTTGTTCTTTGAA 186
QY 181 GAATGAGTCACCTGCTGATGAGATTAAGCAAGTGAACAATTTGCGGAGATAT 240
DB 187 GAATGAGTCACCTGCTGATGAGATTAAGCAAGTGAACAATTTGCGGAGATAT 246
QY 241 TCCGACACCATAGCTAGTTTACAGAGAGCTCAGGCTTCCGCAAGAGACTTGAAGTCA 300
DB 247 TCCGACACCATAGCTAGTTTACAGAGAGCTCAGGCTTCCGCAAGAGACTTGAAGTCA 306
QY 301 AGTCTTGAAGTGTGCTGATCTTTGCTGAAGTGCAGAGTGTGAAGAGAAAGCAAG 360
DB 307 AGTCTTGAAGTGTGCTGATCTTTGCTGAAGTGCAGAGTGTGAAGAGAAAGCAAG 366
QY 361 GACATATATGCTATGAAAGTGAAGAGAGGCTTTATTTGGCCAGAGAGAGGTTTCA 420
DB 367 GACATATATGCTATGAAAGTGAAGAGAGGCTTTATTTGGCCAGAGAGAGGTTTCA 426
QY 421 TTTTGTGAGAGAGCGGAATATTTATCTGAGAGCAAGCCCGTGTATCCCAATTA 480
DB 427 TTTTGTGAGAGAGCGGAATATTTATCTGAGAGCAAGCCCGTGTATCCCAATTA 486
QY 481 CAGTATGCTTTCAAGAGCAAAATCACTTTATCTGATGAGAGATATCAAGCTTGAAGG 540
DB 487 CAGTATGCTTTCAAGAGCAAAATCACTTTATCTGATGAGAGATATCAAGCTTGAAGG 546

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QY 541 GACTTGCTGCTACTTTTGAATAGATATGAGACCACTAGATGAAAACTGATACAGTTT 600
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DB 547 GACTTGCTGCTACTTTTGAATAGATATGAGACCACTAGATGAAAACTGATACAGTTT 606
| | | | |
QY 601 TACTTACGTGAGCTGATTTTGGCTGTTCAAGCTTCATGTATGGAGATACGTGATCGA 660
| | | | |
DB 607 TACTTACGTGAGCTGATTTTGGCTGTTCAAGCTTCATGTATGGAGATACGTGATCGA 666
| | | | |
QY 661 GACATCAAGCTGAGAACATTTCTGTTGACCGCAGGACACATCAAGCTGGTGGATTTT 720
| | | | |
DB 667 GACATCAAGCTGAGAACATTTCTGTTGACCGCAGGACACATCAAGCTGGTGGATTTT 726
| | | | |
QY 721 GGAATCTGCGCGGAAAAATGAATTCAACAGATGATGATGCCAAATCCCGATTTGGAGCC 780
| | | | |
DB 727 GGAATCTGCGCGGAAAAATGAATTCAACAGATGATGATGCCAAATCCCGATTTGGAGCC 786
| | | | |
QY 781 CCAAGATTACATGGCTCTCTGAAGTGTGACTGTATGATGAGGGGATGAAAAAGGCACTTAC 840
| | | | |
DB 787 CCAAGATTACATGGCTCTCTGAAGTGTGACTGTATGATGAGGGGATGAAAAAGGCACTTAC 846
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QY 841 GGCTTGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
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DB 847 GGCTTGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 906
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QY 901 TCCCTCTGCGCAGAGGGAACCTCTGCGCAGAACCTTCAATATGATGATTTCCAGCGG 960
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DB 907 TCCCTCTGCGCAGAGGGAACCTCTGCGCAGAACCTTCAATATGATGATTTCCAGCGG 966
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QY 961 TTTTGAATTTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
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DB 967 TTTTGAATTTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026
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QY 1021 TTGTTGTGCGGCGCAGAAAAAGAGACTGAGTTTGAAGTCTTGTGCGCATGCTTTCTTC 1080
| | | | |
DB 1027 TTGTTGTGCGGCGCAGAAAAAGAGACTGAGTTTGAAGTCTTGTGCGCATGCTTTCTTC 1086
| | | | |
QY 1081 TCTAAATTTGATCTGGAACAACATTTGTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCAAG 1140
| | | | |
DB 1087 TCTAAATTTGATCTGGAACAACATTTGTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCAAG 1146
| | | | |
QY 1141 TCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
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DB 1147 TCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1206
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QY 1201 CCGTCCAGACTGAGCCCTCAGGCTTCTCGGCTGGAAGAACTGCGCTTTGTGGGTTTTCG 1260
| | | | |
DB 1207 CCGTCCAGACTGAGCCCTCAGGCTTCTCGGCTGGAAGAACTGCGCTTTGTGGGTTTTCG 1266
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QY 1261 TACAGCAAGGCACTGGGATTTTGTGTAGATCTGAGTCTGTGTGTGTGTGTGTGTGTGTGT 1320
| | | | |
DB 1267 TACAGCAAGGCACTGGGATTTTGTGTAGATCTGAGTCTGTGTGTGTGTGTGTGTGTGTGT 1326
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QY 1321 CCTGCAAGACTAGCTCCATGGAAGAAACCTTCCATCAAGAAAGAAAGAGTACAAAGC 1380
| | | | |
DB 1327 CCTGCAAGACTAGCTCCATGGAAGAAACCTTCCATCAAGAAAGAAAGAGTACAAAGC 1386
| | | | |
QY 1381 TCTCAGGACAAGTGTCAACAAGT 1403
| | | | |
DB 1387 TCTCAGGACAAGTGTCAACAAGT 1409
| | | | |
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RESULT 4
US-10-238-709-1

Sequence 1, Application US/10238709
Patent No. 6680188
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CLO01164DIV
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11

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NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1515  
TYPE: DNA  
ORGANISM: Human  
US-10-238-709-1  
Query Match 22.6%; Score 1391.8; DB 4; Length 1515;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1396; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 ATGTGAAGTTCAATATGAGACCGGAAATCCTTTGATGATGCTGTGCTGTAACCCATT 60  
| | | | |  
DB 7 ATGTGAAGTTCAATATGAGACCGGAAATCCTTTGATGATGCTGTGCTGTAACCCATT 66  
| | | | |  
QY 61 GCCACCGGCGCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACTTTATGACTCA 120  
| | | | |  
DB 67 GCCACCGGCGCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACTTTATGACTCA 126  
| | | | |  
QY 121 CAGCAGATGCTCTCTTTCCAGAGAGGAAATTAATGATGCTTTGTTCTTTGAA 180  
| | | | |  
DB 127 CAGCAGATGCTCTCTTTCCAGAGAGGAAATTAATGATGCTTTGTTCTTTGAA 186  
| | | | |  
QY 181 GAATGACATGACGCTGCTGATGAGATTAAGACCGTGAACCTTGTCCGGAATAT 240  
| | | | |  
DB 187 GAATGACATGACGCTGCTGATGAGATTAAGACCGTGAACCTTGTCCGGAATAT 246  
| | | | |  
QY 241 TCCGACACCATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
| | | | |  
DB 247 TCCGACACCATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 306  
| | | | |  
QY 301 AGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
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DB 307 AGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 366  
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QY 361 GACATCTATGCTATGAAAGTATGAGAAAGAAAGCTTTATTTGGCCAGAGCAAGTTTCA 420  
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DB 367 GACATCTATGCTATGAAAGTATGAGAAAGAAAGCTTTATTTGGCCAGAGCAAGTTTCA 426  
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QY 421 TTTTGAAGAGAGCGGAACATATTAATCTGAGACAAGCCCGTGGATCCCAATTA 480  
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DB 427 TTTTGAAGAGAGCGGAACATATTAATCTGAGACAAGCCCGTGGATCCCAATTA 486  
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QY 481 CAGATGCTTTTCAAGCAAAAAATCACTTTATGATGAGAGAAATACAGCTGAGAGG 540  
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DB 487 CAGATGCTTTTCAAGCAAAAAATCACTTTATGATGAGAGAAATACAGCTGAGAGG 546  
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QY 541 GACTTGCTGATCACTTTGAATATGAGAGCAAGTTAGATGAAACCTGATACGTTT 600  
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DB 547 GACTTGCTGATCACTTTGAATATGAGAGCAAGTTAGATGAAACCTGATACGTTT 606  
| | | | |  
QY 601 TACTTACGTGAGCTGATTTTGGCTGTTCAAGCTTCATGTATGGAGATACGTGATCGA 660  
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DB 607 TACTTACGTGAGCTGATTTTGGCTGTTCAAGCTTCATGTATGGAGATACGTGATCGA 666  
| | | | |  
QY 661 GACATCAAGCTGAGAACTTCTGTTGACCGCAGGACACATCAAGCTGGTGGATTTT 720  
| | | | |  
DB 667 GACATCAAGCTGAGAACTTCTGTTGACCGCAGGACACATCAAGCTGGTGGATTTT 726  
| | | | |  
QY 721 GGAATCTGCGCGGAAAAATGAATTCAACAGATGATGATGCCAAATCCCGATTTGGAGCC 780  
| | | | |  
DB 727 GGAATCTGCGCGGAAAAATGAATTCAACAGATGATGATGCCAAATCCCGATTTGGAGCC 786  
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QY 781 CCAAGATTACATGGCTCTCTGAAGTGTGACTGTATGATGAGGGGATGAAAAAGGCACTTAC 840  
| | | | |  
DB 787 CCAAGATTACATGGCTCTCTGAAGTGTGACTGTATGATGAGGGGATGAAAAAGGCACTTAC 846  
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QY 841 GGCTTGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
| | | | |  
DB 847 GGCTTGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 906  
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QY 901 TCCCTCTGCGCAGAGGGAACCTCTGCGCAGAACCTTCAATATGATGATTTCCAGCGG 960  
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Db 907 TCCCCCTGCAAGGAACTCTGCGAGAACCTTCAATTAATGATTTCCAGCGG 966
QY 961 TTTTGAATTTTCAATGACCCCAAAAGTACGACGACTTTCTGATCTGATTCAAAGC 1020
Db 967 TTTTGAATTTTCAATGACCCCAAAAGTACGACGACTTTCTGATCTGATTCAAAGC 1026
QY 1021 TTTTGGGGGGGAGAAAGAGACGTAAGTTGAAAGTCTTGGCCATCCCTTCTTC 1080
Db 1027 TTTTGTGGGGGAGAAAGAGACGTAAGTTGAAAGTCTTGGCCATCCCTTCTTC 1086
QY 1081 TCTAAATTTGACTGGAACAACATTCGTAATCTCTCCCTTCGTTCCCACTCAAG 1140
Db 1087 TCTAAATTTGACTGGAACAACATTCGTAATCTCTCCCTTCGTTCCCACTCAAG 1146
QY 1141 TCTGACGATGACACCTTCATTTTGTATGAACGAGAGAAATTCGTGGGTTTCATCTCT 1200
Db 1147 TCCGACGATGACACCTTCATTTTGTATGAACGAGAGAAATTCGTGGGTTTCATCTCT 1206
QY 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGTTGAAAGAACTGCGCTTGTGGGGTTTCG 1260
Db 1207 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGTTGAAAGAACTGCGCTTGTGGGGTTTCG 1266
QY 1261 TACAGCAAGGCACTGGGGATTTCTTGTAGATCTGAGCTGTGTGCGGGTCTGAGCTCC 1320
Db 1267 TACAGCAAGGCACTGGGGATTTCTTGTAGATCTGAGCTGTGTGCGGGTCTGAGCTCC 1326
QY 1321 CCGTGCAGCACTGAGCTTCATGAAAAAACTTCTCATMAAGCAAGGCTTCAAGAC 1380
Db 1327 CCGTGCAGCACTGAGCTTCATGAAAAAACTTCTCATMAAGCAAGGCTTCAAGAC 1386
QY 1381 TCTCAGGACAAAGTGTCAAGAT 1403
Db 1387 TCTCAGGACAAAGTGTCAAGAT 1409

RESULT 5

US-09-774-528-419

/ Sequence 419, Application US/09774528
/ Patent No. 6743619
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Zhou, Ping
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Abundi, Vinod
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Zhang, Jie
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Drmanac, Radote T.
/ TITLE OF INVENTION: No. 6743619el Nucleic Acids and
/ FILE REFERENCE: Polypeptides
/ CURRENT APPLICATION NUMBER: US/09/774, 528
/ CURRENT FILING DATE: 2001-01-30
/ NUMBER OF SEQ ID NOS: 441
/ SOFTWARE: pc_fl_genes Version 2.0
/ SEQ ID NO 419
/ LENGTH: 2162
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (364)..(2010)
US-09-774-528-419

Query Match 15.5%; Score 952.4; DB 4; Length 2162;
Best Local Similarity 99.4%; Pred. No. 3.9e-256;

Matches 956; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGTTAAATTTCAATATGAGACCGGGAATCTCTTGGATGCTGTGCTGTGAACCCATT 60
Db 364 ATGTTAAATTTCAATATGAGACCGGGAATCTCTTGGATGCTGTGCTGTGAACCCATT 423
QY 61 GCCAGCCGGGCTCCAGGCTGATCTGTCTTCCAGGGGAAACCACTTTATGACTCA 120
Db 424 GCCAGCCGGGCTCCAGGCTGATCTGTCTTCCAGGGGAAACCACTTTATGACTCA 483
QY 121 CAGCAGATGCTCTCTTTTCCGAGAGGGAATATAGATGCCCTTTGTCTTTGAA 180
Db 484 CAGCAGATGCTCTCTTTTCCGAGAGGGAATATAGATGCCCTTTGTCTTTGAA 543
QY 181 GAATGAGTCAAGCTCTCTTGTATGAAGATTAAGCAGTGAACACTTTGTCCGGAAGTAT 240
Db 544 GAATGAGTCAAGCTCTCTTGTATGAAGATTAAGCAGTGAACACTTTGTCCGGAAGTAT 603
QY 241 TCCGACACCATAGCTGAGTTTACAGGAGCTCCAGCCCTTCCGCAAAAGACTTCGAGTCAGA 300
Db 604 TCCGACACCATAGCTGAGTTTACAGGAGCTCCAGCCCTTCCGCAAAAGACTTCGAGTCAGA 663
QY 301 AGCTTTGATGATGCTGATCTTGTGCTGAAGTGAAGTGTAAAGAGAAACCAACCGG 360
Db 664 AGCTTTGATGATGCTGATCTTGTGCTGAAGTGAAGTGTAAAGAGAAACCAACCGG 723
QY 361 GACATCTATGCTATGAAGTGAAGAAAGGCTTTATTTGGCCCAAGAGAGGTTTCA 420
Db 724 GACATCTATGCTATGAAGTGAAGAAAGGCTTTATTTGGCCCAAGAGAGGTTTCA 783
QY 421 TTTTGTAGAGAGAGGGAACATATATCTGAAAGCAAGGCCGCTGATCCCAATTA 480
Db 784 TTTTGTAGAGAGAGGGAACATATATCTGAAAGCAAGGCCGCTGATCCCAATTA 843
QY 481 CAGTATGCTTTCAAGACAAATAATCACTTTATCTGATGAGAGAAATATCAGCTGAGG 540
Db 844 CAGTATGCTTTCAAGACAAATAATCACTTTATCTGATGAGAGAAATATCAGCTGAGG 903
QY 541 GACTTGCTGTCACTTTTGAATATGATATGAGACCACTTATGATGAAACCTGATACAGTTT 600
Db 904 GACTTGCTGTCACTTTTGAATATGATATGAGACCACTTATGATGAAACCTGATACAGTTT 963
QY 601 TACCTAGCTGAGCTGATTTTGGCTGTCAAGGCTTCAATCTGATGAGATGAGCTGAGA 660
Db 964 TACCTAGCTGAGCTGATTTTGGCTGTCAAGGCTTCAATCTGATGAGATGAGCTGAGA 1023
QY 661 GACATCAAGCTCAGAACATTTCTGTTGACCGCAGACAGACATCAAGCTGTGATTTT 720
Db 1024 GACATCAAGCTCAGAACATTTCTGTTGACCGCAGACAGACATCAAGCTGTGATTTT 1083
QY 721 GATCTGCGCGGAAATGAAATCAAAAGATGTTGAATGCCAACTCCGATTTGGGACC 780
Db 1084 GATCTGCGCGGAAATGAAATCAAAAGATGTTGAATGCCAACTCCGATTTGGGACC 1143
QY 781 CCAGATTCATAGCTCTCCGAAGTGTGAGTGAACGCGGAGTGAAGGCAAGCTTAC 840
Db 1144 CCAGATTCATAGCTCTCCGAAGTGTGAGTGAACGCGGAGTGAAGGCAAGCTTAC 1203
QY 841 GGCCTGACTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 900
Db 1204 GGCCTGACTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1263
QY 901 TCCCTCTTCCAGAGGAACTTCTCCAGAACCTTCAATATGATGATTTTCCAGCGG 960
Db 1264 TCCCTCTTCCAGAGGAACTTCTCCAGAACCTTCAATATGATGATTTTCCAGCGG 1323
QY 961 TT 962
Db 1324 TT 1325

RESULT 6

US-09-916-204-1

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; Sequence 1, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1133
; TYPE: DNA
; ORGANISM: Human
US-09-916-204-1

Query Match      12.2%; Score 750; DB 4; Length 1133;
Best Local Similarity 99.3%; Pred. No. 1.6e-199;
Matches 753; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGTGAAGTTCAAAATATGAGCGCGGAATCCTTTGATGCTGTGCTGTAACCATTT 60
DB 54 ATGTGAAGTTCAAAATATGAGCGCGGAATCCTTTGATGCTGTGCTGTAACCATTT 113
QY 61 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATGACTCA 120
DB 114 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATGACTCA 173
QY 121 CAGCAGATGTCCTCTCTTTCCGAGAAAGGATATAGATGCCCTTTGTTCTTTGAA 180
DB 174 CAGCAGATGTCCTCTCTTTCCGAGAAAGGATATAGATGCCCTTTGTTCTTTGAA 233
QY 181 GAATGAGTCAGGCTGCTGATGAGATTAAGCAACGTAGCACTTTTCCGGAAGTAT 240
DB 234 GAATGAGTCAGGCTGCTGATGAGATTAAGCAACGTAGCACTTTTCCGGAAGTAT 293
QY 241 TCCGACACCATATGCTGAGTTAAGAGAGCTCCAGCCTTCGGCAAGAGACTTCGAACTCAGA 300
DB 294 TCCGACACCATATGCTGAGTTAAGAGAGCTCCAGCCTTCGGCAAGAGACTTCGAACTCAGA 353
QY 301 AGCTTTGATGCTGTGCTGCTCACTTTGCTGAAGTGCAGGTGCTAAGAGAGAAACCAACCGGG 360
DB 354 AGCTTTGATGCTGTGCTGCTCACTTTGCTGAAGTGCAGGTGCTAAGAGAGAAACCAACCGGG 413
QY 361 GACATCTATGCTATGAAAGTATGAGAGAGAGGCTTTATTTGGCCGAGAGAGGTTTCA 420
DB 414 GACATCTATGCTATGAAAGTATGAGAGAGAGGCTTTATTTGGCCGAGAGAGGTTTCA 473
QY 421 TTTTGTGAGAAAGACCGGAACATATTATCTCGAAGCAACAAGCCGCTGTGATCCCAATTCA 480
DB 474 TTTTGTGAGAAAGACCGGAACATATTATCTCGAAGCAACAAGCCGCTGTGATCCCAATTCA 533
QY 481 CAGTATGCCCTTCAGAGCAAAATATCACTTTATCTGATGAGAGATATCAAGCTTGAAGGG 540
DB 534 CAGTATGCCCTTCAGAGCAAAATATCACTTTATCTGATGAGAGATATCAAGCTTGAAGGG 593
QY 541 GACTTGCTGTCACTTTTGAATAGATATGAGAGCAGTATGAGAAACCTGATACAGTTT 600
DB 594 GACTTGCTGTCACTTTTGAATAGATATGAGAGCAGTATGAGAAACCTGATACAGTTT 653
QY 601 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCACTTGATGGAGTACGTGCATGA 660
DB 654 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCACTTGATGGAGTACGTGCATGA 713
QY 661 GACATCAAGCTGAGAACATTTCTGTTGACCGCAACAGGACACATCAAGCTGTGATTTT 720
DB 714 GACATCAAGCTGAGAACATTTCTGTTGACCGCAACAGGACACATCAAGCTGTGATTTT 773
QY 721 GGATCTGCCGCGAAATGAAATTCACAAAGATGTGAA 758
DB 774 GGATCTGCCGCGAAATGAAATTCACAAAGATGTGAA 811
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```
RESULT 7
US-10-282-048-1
; Sequence 1, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1133
; TYPE: DNA
; ORGANISM: Human
US-10-282-048-1

Query Match      12.2%; Score 750; DB 4; Length 1133;
Best Local Similarity 99.3%; Pred. No. 1.6e-199;
Matches 753; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGTGAAGTTCAAAATATGAGCGCGGAATCCTTTGATGCTGTGCTGTAACCATTT 60
DB 54 ATGTGAAGTTCAAAATATGAGCGCGGAATCCTTTGATGCTGTGCTGTAACCATTT 113
QY 61 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATGACTCA 120
DB 114 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATGACTCA 173
QY 121 CAGCAGATGTCCTCTCTTTCCGAGAAAGGATATAGATGCCCTTTGTTCTTTGAA 180
DB 174 CAGCAGATGTCCTCTCTTTCCGAGAAAGGATATAGATGCCCTTTGTTCTTTGAA 233
QY 181 GAATGAGTCAGGCTGCTGATGAGATTAAGCAACGTAGCACTTTTCCGGAAGTAT 240
DB 234 GAATGAGTCAGGCTGCTGATGAGATTAAGCAACGTAGCACTTTTCCGGAAGTAT 293
QY 241 TCCGACACCATATGCTGAGTTAAGAGAGCTCCAGCCTTCGGCAAGAGACTTCGAACTCAGA 300
DB 294 TCCGACACCATATGCTGAGTTAAGAGAGCTCCAGCCTTCGGCAAGAGACTTCGAACTCAGA 353
QY 301 AGCTTTGATGCTGTGCTGCTCACTTTGCTGAAGTGCAGGTGCTAAGAGAGAAACCAACCGGG 360
DB 354 AGCTTTGATGCTGTGCTGCTCACTTTGCTGAAGTGCAGGTGCTAAGAGAGAAACCAACCGGG 413
QY 361 GACATCTATGCTATGAAAGTATGAGAGAGAGGCTTTATTTGGCCGAGAGAGGTTTCA 420
DB 414 GACATCTATGCTATGAAAGTATGAGAGAGAGGCTTTATTTGGCCGAGAGAGGTTTCA 473
QY 421 TTTTGTGAGAAAGACCGGAACATATTATCTCGAAGCAACAAGCCGCTGTGATCCCAATTCA 480
DB 474 TTTTGTGAGAAAGACCGGAACATATTATCTCGAAGCAACAAGCCGCTGTGATCCCAATTCA 533
QY 481 CAGTATGCCCTTCAGAGCAAAATATCACTTTATCTGATGAGAGATATCAAGCTTGAAGGG 540
DB 534 CAGTATGCCCTTCAGAGCAAAATATCACTTTATCTGATGAGAGATATCAAGCTTGAAGGG 593
QY 541 GACTTGCTGTCACTTTTGAATAGATATGAGAGCAGTATGAGAAACCTGATACAGTTT 600
DB 594 GACTTGCTGTCACTTTTGAATAGATATGAGAGCAGTATGAGAAACCTGATACAGTTT 653
QY 601 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCACTTGATGGAGTACGTGCATGA 660
DB 654 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCACTTGATGGAGTACGTGCATGA 713
QY 661 GACATCAAGCTGAGAACATTTCTGTTGACCGCAACAGGACACATCAAGCTGTGATTTT 720
DB 714 GACATCAAGCTGAGAACATTTCTGTTGACCGCAACAGGACACATCAAGCTGTGATTTT 773
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Dy 721 GGATCTGCCCGGAAATGTAATTCAACAGATGGTGA 758
|||
Db 774 GGATCTGCCCGGAAATGTAATTCAACAGATGGTGA 811

RESULT 8

```

US-09-016-434-513
Sequence 513, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 513:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINNO01
CLONE: 2290031
US-09-016-434-513

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Query Match : 4.28; Score 258; DB 4; Length 258;

QY	5051	CCAAAGTCGTATTTCTCGGCTACAAACGAAA	CTCAGAGAAATTA	CTGCATCCGGAAAGGA	5110
Db	1	GCANAATGTCATTTCTCCGCTACAAACGAAA <td>CTCAGAAATTA <td>CTGCATCCGGAAAGGA</td> <td>60</td> </td>	CTCAGAAATTA <td>CTGCATCCGGAAAGGA</td> <td>60</td>	CTGCATCCGGAAAGGA	60
QY	5111	TAGAGACCTCGAGCCCTGCAGCTGTATCCA	CTTCCACCAATTA	CTCAGTATCTCATTTGGA	5170
Db	61	TAGAGACCTCGAGCCCTGCAGCTGTATCCA	CTTCCACCAATTA	CTCAGTATCTCATTTGGA	120
QY	5171	CCATTAATTTCTAGGAATCGACATGAAGCAGTAC	ACGCTGAGGAAATTTCTG	GATTAAGA	5230
Db	121	CCATTAATTTCTAGGAATCGACATGAAGCAGTAC	ACGCTGAGGAAATTTCTG	GATTAAGA	180
QY	5231	ATGACCAATTCCTTGGACCTGCTGTGTTTGG	CGCGCTCTTCCAACA	CGCTTCCCTGTCTGA	5290
Db	181	ATGACCAATTCCTTGGACCTGCTGTGTTTGG	CGCGCTCTTCCAACA	CGCTTCCCTGTCTGA	240

Qy	5291	TCGTGAGGTGAACAGCG	5308
Db	241	TCGTGAGGTGAACAGCG	258

RESULT 9

```

US-09-949-016-2640
; Sequence 2640, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/0241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2640
; LENGTH: 2423
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-2640

```

Query Match	3.74;	Score 228.2;	DB 4;	Length 2423;
Best Local Similarity	52.24;	Pred. No. 8.6e-53;		
Matches 587; Conservative	0;	Mismatches 523;	Indels 15;	Gaps 3;

QY	152	TATTAGATGCCCTCTTGGTCTCTTTGAAAGATGCACTCAGCCGCTGTGATGAAGATTA	211
Db	1021	TACTGATATATCTCATCTGCCTTTATATGATGATGCATTAATCTCCATTGAGGAAGAGA	10808
QY	212	AGCAGTGAACACTTTGTCCGGAGTATTCGACACCATATGCTGAGTTACAGAGCTCC	271
Db	1081	AGAACTATCTCGAATACCTTAAGATGGGCTAAACCATTACTCTTAAGGTGAACAAATGC	1140
QY	272	AGCCTTCGGGAAAAGCACTTGAAAGTCAGAAAGTCGTATAGGTGTGGATCACTTGCTAG	331
Db	1141	GATTACATAGAGAAAGCTTTGAAATATTTAAAGTGATTTGGTCGAGAGCTTTGGGAGG	1200
QY	332	TGCAGTGTATAGAGAAAGCAACCGGGACATCTATGCTATGAAAGTATGAAGAAGA	391
Db	1201	TTTGCTGTATGTAATCTAAAAAATGCAATAAAGTGTTCGCATGAAAAATATGTAATAAAT	1260
QY	392	AGGCTTTATTTGGCCCGAGAGACGGTTTCATTTTGTAGAGAAAGCGGACATATTAATCTC	451
Db	1261	GGGAAATGCTGAAGAAAGCTGAGCAGCAGTATTTTCGTGAAGAAAGGATGTAATTAATGA	1320
QY	452	GAAGCAACAAGCCGCTGATCCCCCAATTACAGTATGCTTTCAGAGCAAAAATCACTTT	511
Db	1321	ATGAGAGCAATTAATGATATTAACAACCTTGCACTATGCTTTCAGAGATGACAAATTAATAT	1380
QY	512	ATCTGATGAGGAATATCAGCTCTGAGGGGACCTTGCTGCACTTTGATATGATATGAGG	571
Db	1381	ACCGTGTTATGATTAATTAATGTTGGTGGGATTTGCTACTCTACTCAGCAAAATTTGAG	1440
QY	572	ACCACTTAAGATGAAGAAACCTGATACAGTTTAACTAGCTGAGCTGATTTGGCTGTCA	631
Db	1441	ATAGATTTGCTGAAGATATGCTGATTAATTTACTTGGCTGAGATGTGATATGCAATTAAGCT	1500
QY	632	GCGTTTCATCTGATGGGATACGTGCATCGAGACATCAAGCTGAGAACATTTCTCGTGAAC	691
Db	1501	CAGTTTCATCAGCTACATTAATGTACACAGAGCAATTAACCTGACCAATATATCTGATGA	1560
QY	692	GCACAGACATCAAGCTGTGATTTTGGATCTGCCGGAAAAATGAATTCAAACAAGA	751

Db 1561 TGAATGACATATTCGGTTAGACAGATTTTGTTCTTGCTGAAGCTGATGGAAGATGAA 1620
Qy 752 TGGTGAATCCCAACTCCCGATTGGGACCCAGATTACATGGCTCTGAAAGTGTGACTG 811
Db 1621 CGGTTCAGTCCCTCAGGCGCTGAGAACTCCAGATATATCTCTCTGAAATCTTTCAAG 1680
Qy 812 TGATGAACGGGGATGGAAAAAGGACCTAGGGCTGAGCTGTGACTGTGTGCTGAGGGG 871
Db 1681 CCAATGAG--ATGAAAAAGGAGATATGAGACTGATGATGATGCTGTGTGCTTTGGGG 1737
Qy 872 TGAATGCTATGAGATGATTTATGAGAGATCCCTCTTCCAGAGGAACTCTGCCAGAA 931
Db 1738 TCTGTATGATGAAATGCTTTACGGAGAAACACATTTATGAGAAATGCTGTGGAGA 1797
Qy 932 CCTTCATATACATTAATGAATTTCCAGCGGTTTGAATTTCCAG--ATGACCCCAAG 988
Db 1798 CATACGAAAAATCATGAACCAAGAGAGGTTTCAAGTTTCCAGGCCCAAGTGAATGATG 1857
Qy 989 TGAGCAGTACTTTTGTGATCTGATTCAGAAAGCTTGTGTGGCGCCAGAAAGAGAGCT-- 1046
Db 1858 TGTTCGAAAAATGCTAAGATCTTATTCGAAAGGCTCATTTGTAGAGAGAACTGCACTTG 1917
Qy 1047 -----GAAGTTGAAGGCTTTTCTGTCGCATCTTTCTTCTTAAATTTGACTGGAGA 1099
Db 1918 GTCAAAATGGAATGAAAGCTTTAAGAAACACCATTTTCACTGGAATTTGATTTGGATA 1977
Qy 1100 ACATTTGTAATCTCTCTCCCTCTTCTTCCACCTCAAGTCTGAGTGAACACTTCCA 1159
Db 1978 AATATTCGAACTGTGAAGCACTTATATTCAGAACTGTAGAGCCCAAGATACATGCA 2037
Qy 1160 ATTTGATGAACAGAGAAATGCTGGGTTTCATCTCCCTGCTGCGCAGCTGAGCCCT 1219
Db 2038 ATTTGATGATGATGATGATGATTTTAAAAAATTTGAAACGATGCCCAACCAACATTA 2097
Qy 1220 CAGGCTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTCTGACA 1264
Db 2098 CTGCATTTTCTGGCCACCATCTGCCATTTGTGTTTACATATA 2142

RESULT 10
US-08-422-699A-12
Sequence 12, Application US/08422699A
Patent No. 5955265
GENERAL INFORMATION:
APPLICANT: Brook, J. David
APPLICANT: Housman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen G.
APPLICANT: Johnson, Keith J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,699A
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612

FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-422-699A-12

Query Match 3.6%; Score 220.8; DB 2; Length 2726;
Best Local Similarity 53.7%; Pred. No. 1.1e-50;
Matches 531; Conservative 0; Mismatches 442; Indels 15; Gaps 3;

Qy 194 CTGCTGTGATGAAGTTTAAGCAGTGAACACTTTGTCCGAAATTTCCAGACACATAG 253
Db 243 CCGAATCGGCCAGACAAAGTACGTGGCCGACTTCTTCAAGTGGCGAGAGCCCATCGTG 302
Qy 254 CTGAATTCAGAGGCTCAGGCTTGCGCAAGGACTTGAAGTCAAGATCTTGAAGTT 313
Db 303 TGAGGCTTAAAGAGGTTCCGATCTGCAGAGGAGCACTTTCGAAATTTGAAAGTATCG 362
Qy 314 GTGTCACTTTGCTGAGTGAAGTGAAGTGTGAAGAGAAAGCAACCGGGAGCATATATGCTA 373
Db 363 GCGGGGCGTTTACGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 422
Qy 374 TGAAGTGAAGAAAGAGGCTTTATGAGCCAGAGCAAGTTTATTTTGAAGAG 433
Db 423 TGAAGATCATGAACAAAGTGGGACATCTGAAGAGGGGAGAGGTGTGCTTCCGTGAGG 482
Qy 434 AGCGAATATATATCTGGAAGCAAGCAAGCCGTTGATCCCCAATTACAGTATGCTTTC 493
Db 483 AAGGGAAGTGTGATGATGAGGAGCCGCGGTGATCAAGCTGCACTTCCGCTTCC 542
Qy 494 AGGCAAAATCACTTTATCTGATGAGAGATATCAAGCTGAGAGGGAATTTGCTGTGAC 553
Db 543 AGGATGAGAACTACCTGATACGTGTGATGATTAAGTGGCGGGAGCTGTGACAC 602
Qy 554 TTTGAATATGATATGAGAGCAAGTATGATGAAGAACTGATATACATTTTAACTAGTGA 613
Db 603 TGCTAGGCAAGTTTGGGAGAGGAGTTCGCGCGAATGAGCGGCTTCACTGCGGAGAGA 662
Qy 614 TGAATTTGGCTGTACAGCGCTTCACTGATGAGATGAGTATGATGAGATCAATCAAGCTG 673
Db 663 TTGTATGCGCATATGATCTGCGGTGACCGGCTTGGCTTATGATGACAGGAGATCAAAACCG 722
Qy 674 AGAATTTCTGTTGACCGCAGAGCAATCAAGCTGTGATTTTGAATCTGCGCGGA 733
Db 723 ACAATCTCTGTGAGCCGCTGTGGCAATCCGCTGCGGCACTTCCGCTTTCCTCA 782
Qy 734 AATGAATTTCAACAAAGATGTTGAATGCAAACTCCGATTTGGAGCCCAATTTCAATG 793
Db 783 AGCTCGGGCAGATGAACGTTGCGGTGCTGTGTGGCTGTGTGGCCACCCAGACTACCTGT 842
Qy 794 CTCCTGAAGTGTGA---CTGTGATGAACGGGGAATGAAAAAGGACCTTACGGGCTGACT 850

Db 843 CCCCCGATCTCGACGGCTGTGGGCGGTGGGCGAGCAGCAGCTACGGGCGGAGT 902
QY 851 GTGACTGTGTGTGACATGAGGCGGTGATTTGCTATGATGATTTATGGAGATCCCGCTTCG 910
Db 903 GTGACTGTGTGTGAGGCGGTGTATTTCCCTATGAAATGTTCTATGAGGCGAGACCCCTTCT 962
QY 911 CAGAGGAACTCTGCGAGAACCTTCAATTAATGATTTGCAAGCGGTTTGTAAAT 970
Db 963 ACACGATTTCCAGCGCGGAGACCTATGCGAAGATGTCCTACAMAGACACCTCTCTC 1022
QY 971 TTCAGATGACCCCAAGTGAAGT---GACTTTCTGATCTGATTTCAAGCTTTGT 1027
Db 1023 TGCGGCTGTGAGAGAGGCGGTCCCTGAGAGGCTGAGACTTCACTTCAAGGTTGCTGT 1082
QY 1028 GCGGCCAGAAAGAGACTGAAGTTGAAGCTTTGCTC-----CATCTTCT 1078
Db 1083 GTCCCCCGAGACAGCGCTGGCGGCGGTGAGACAGCGACTTCCGACACATCCCTTCT 1142
QY 1079 TCTCTAAATGACTGAGACATTTGTAATCTCTCTCCCTTCTGTTCCACCTCA 1138
Db 1143 TCTTGGCTTCACTGGAGTGTCTCCGAGACAGCGTGTCCCTTTACACCGGATTTG 1202
QY 1139 AGTGTGACGATGACACCTCCCAATTTGA 1166
Db 1203 AAGTCCACCGACACATGCACTTCA 1230

RESULT 11
US-08-422-7068-12
Sequence 12, Application US/08422706B
Patent No. 5977333
GENERAL INFORMATION:
APPLICANT: Brook, J. David
APPLICANT: Housman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen G.
APPLICANT: Johnson, Keith J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-422-7068-12
Query Match 3.6%; Score 220.8; DB 2; Length 2726;
Best Local Similarity 53.7%; Pred. No. 1.1e-50;
Matches 531; Conservative 0; Mismatches 442; Indels 15; Gaps 3;
QY 194 CTGCTGTATGAAATTAAGACGTGAGCACTTGTCCGAAATTCGACACCATAG 253
Db 243 CCGAAGTGGCCAGGACAAAGTACGTGCGCATTCCTTGACATGAGGCGGAGCCATGCTG 302
QY 254 CTGAGTTACAGAGCTCCAGCCTTGGCGAAAGACTTGAAGTCAAGTCTTGAAGTT 313
Db 303 TGAGGCTTAAGAGGCTCCAGTCGACAGAGGACGACTTGAATTCGAAGGTAATCGAC 362
QY 314 GTGCTCACTTGTCTGAGTGTGAGTGTGAAGAGAAAGCAACCGGCGCATCTATGCTA 373
Db 363 GCGGGCGCTTACAGCAGAGTACGCGTATGTAATGAAGACAGCGGCGGATGATGCCA 422
QY 374 TGAAGTATGAAAGAAAGGCTTTATTGCGCCAGAGAGGCTTTCAITTTTGAAGAG 433
Db 423 TGAAGATCATGAACAAGTGGGACATGCTGAAGAGGCGGCGAGGTGCTTCCGAGAG 482
QY 434 AGCGAACAATATTATCTGCAACACAGCGCCGTGATCCCAATTAAGTATGCTTTC 493
Db 483 AAGGGACGCTGTGTGAATGAGGACCGCGGTGATCAAGAGCTGCACTTCCGCTTCC 542
QY 494 AGGACAAATACACTTATCTGATGAGAAATATCAGCGCTGAGGCGGACTTGTCTAC 553
Db 543 AAGATGAGAACTACCTGATCTGTGATGATGATATTAAGTGGCGGAGACTGTGACAC 602
QY 554 TTTGAATGATATGAGACCAAGTTAGTGAATAAAGCTGATACGTTTACCTAGTGAC 613
Db 603 TCTGAGCAAGTTGGGAGCGGATTCGCGCGAGATGGCGGCTTCTACCTGGCGAGA 662
QY 614 TGAATTTGCTGTTCACAGCGTTCACTGATGAGATACGTGATGAGACATCAAGCTTG 673
Db 663 TTGTCAATGCGCATGACCTGCGTGCACCGGCTTGGCTACCTGACAGGACATCAACCCG 722
QY 674 AGAACAATCTGTTGACCGCACAGGACATCAAGTGTGATTTGATCTGCGCGCA 733
Db 723 ACAACATCTGCTGAGACCGCTGTGCGACATCTGCGGCGCATCTTGGCTTCTGCTCA 782
QY 734 AATGAATTCAAACAAGATGATGAATGCCAACTCCGATTGCGAATCCGAGTTACATG 793
Db 783 ACTGCGGCGCATGAGAACGATGCGGATGCTGTGTGCTGTGCGACCCAGACTACCTGT 842
QY 794 CTCTGAAAGTCTGA---CTGTGATGAACGGGAGATGAAAAGGACCTACGGCTGAGCT 850
Db 843 CCCCCGAGTCTCGACAGGCTGTGGCGGCTGGGCGTGGGACAGGACTACCGGCGCGAGT 902
QY 851 GTGACTGTGTGTGACATGAGGCGGTGATTTGCTATGATGATTTATGGAGATCCCGCTTCG 910
Db 903 GTGACTGTGTGTGAGGCGGTGTATTTCCCTATGAAATGTTCTATGAGGCGAGACCCCTTCT 962
QY 911 CAGAGGAACTCTGCGCAGAACCTTCAATTAATGATTTGCAAGCGGTTTGTAAAT 970
Db 963 ACACGATTTCCAGCGCGGAGACCTATGCGAAGATGTCCTACAMAGACACCTCTCTC 1022

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OY      9711 TTCCGATGACCCCAAAGTGAGCACT---GACTTTCTTGANTGTATTTAAAGCTTGTGT 1027
Db      1023 TCCCTCTGTGTGACGACAAAGGCTTCCTTGAGAGAGCTCGAGACTTCACTTACGCGGTTCGT 1082
OY      1028 GCGGCGCAAGAAAGAGACTGAAGTTTGAAGTCTTTGCTGC-----CATCCTTCT 1078
Db      1083 GTCCCCCGGAGACACGCGCTGGGCGGGGTGGAGCAGGCGACCTTCCGACATCCCTTCT 1142
OY      1079 TCTCTAAANTGACTGTGAACAACAATTGTAATCTCTCTCCCCCTTGTCTTCCACCTCTGA 1138
Db      1143 TCTTTGGCTTGACTGGAGATGGTCTCCGGGACAGCGTGCCTCCCTTTACACCGGATTTCCG 1202
OY      1139 AGCTGACGATGACCACTTCATTTTGA 1166
Db      1203 AAGTGCCACCGACACATGCAACTTCGA 1230

RESULT 12
US-08-422-699A-8
; Sequence 8, Application US/08422699A
; Patent No. 5955265
; GENERAL INFORMATION:
; APPLICANT: Brook, J. David
; APPLICANT: Housman, David E.
; APPLICANT: Shaw, Duncan J.
; APPLICANT: Harley, Helen G.
; APPLICANT: Johnson, Kelth J.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
; TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02713

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: 'Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,699A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

```

	LENGTH: 2511 base pairs
/	TYPE: nucleic acid
/	STRANDEDNESS: double
/	TOPOLOGY: linear
/	MOLECULE TYPE: DNA (genomic)
/	FEATURE:
/	NAME/KEY: CDS
/	LOCATION: 1..1746
/	US-08-422-699A-8

Query Match	3.5%;	Score 214;	DB 2;	Length 2511;
Best Local Similarity	54.2%;	Pred. No. 8.6e-49;		
Matches 508;	Conservative 0;	Mismatches 415;	Indels 15;	Gaps 3
QY	244	GACACCATGCTGAGTTACAGGAGCTCCGACCTTCGGCAAAAGACTTGGAACTGACGAAGT	303	
DB	43	GCCATGCTGTGTAGAGCTTTAAGAGAGTCCGACTGTCAGAGGAGACGACTTTCGAGATTCTGAA	102	
QY	304	CTTTAGAGTTGTGTCTACTTTTGTCTGAAAGTCAGGTGTGAAGAGAAAGCAACCGGGAGC	363	
DB	103	GTGATTCGAGCGGGGCGCTTCACGAGGTAGCGGTAGTGAATGAAGACACGGGGCAG	162	
QY	364	ATCTATGCTATGAAGAATGATGAAGAAGAGCCTTTATTTGGCCAGAGACAGTTTCAATT	423	
DB	163	GTGTATGCTATGAAGATCATGAACAAGTGGACATGCTGAAGAGAGGCGAGGTGTCTGTC	222	
QY	424	TTTGAAGAAAGCGGAAATATTATCTGAAAGACAAAGCCGTGATCCCCAATTACG	483	
DB	223	TTCCGTGAGAGAGGAGCGTGTGTGATGATGGAGACCGGCGTGTGATCAGAGCTGCAC	282	
QY	484	TATGCGCTTTCAGAGCAAAAATCACTTTATCTGATGAGAAATATACCTGAGAGGAGC	543	
DB	283	TTTCGCTTTCAGAGAGAAATCACTCTGATCTGTCAATGAGATATTACGTGGCGGGAGC	342	
QY	544	TTGCTGTCACTTTGAATAGATATATGAGGACAGTATGATGAAGAACTGATACGTTTAC	603	
DB	343	CTGCTGACATCTGTAGCAAGTTTGGAGAGCGGATTTCCGGCCGAGATGGCGCTTCTAC	402	
QY	604	CTAGCTGACTGATTTTGGCTGTTCACAGCGTTATCTGATGGATACGTGCATCGAGAC	663	
DB	403	CTGGGGAGATGTGATCATGCGCATGACATCGGTGCACCGGCTTGGCTGATGTCACAGGAGC	462	
QY	664	ATCAAGCCCTGAGAAACATTCTGCTGACCGGACAGGACATCAACAGCTGTGATTTTGA	723	
DB	463	ATCAAAACCGACAAACATCTCTGTGACCGCTGTGGCAATTCGCTGGCCGACATTTGCGC	522	
QY	724	TCTGCGCGGAAATGAATTCAACAAGATGCTGATGCAAACTCCGATTGGGACCCCA	783	
DB	523	TCTTGCTCAAGCTGCGGGCAGATGAAACGGTGGCGGTGCTGTGGCGCTGTGGCACCCCA	582	
QY	784	GATTTCATGGCTCTCGA---AGTCTGACTGTGATGAACGGGGATGCAAAAGGCACTTAC	840	
DB	583	GACTACCTGTCTCCCGAGATCTCTCAGCGTGTGGCGCGGTGGGACCGGACAGCTTAC	642	
QY	841	GGCCTGAGCTGTGACTGGTGTGACTGGGCGTGAATTTGCTATGATGATTTATGGGAGA	900	
DB	643	GGGCGCGAGTGTGACTGGTGGCGCTGGGTGTATTCCGCTATGAATGTTTATGGGAG	702	
QY	901	TCCCCCTTGCAGAGGGAACCTTGGCCAGAACCTTCAATTAATATGAAATTTCCAGCG	960	
DB	703	ACGCGCTTCTACGGGAGATTCCAACGGCGGAGACCTATGGCAAGATGTCCTACAAAGAG	762	
QY	961	TTTTTGAATTTTCAGATGAACCCCAAGGTGACAGT---GACTTTCTTGAATTCGATTCGA	1017	
DB	763	CACCTTCTCTGCGCGCTGTGGAGCAAGAGGGTCCCTTAGAGAGGCTTCGAACTTATTAC	822	
QY	1018	AGCTGTGTGTGCGGACGAAAGAGAGACTGAAGTTTGAAGTCTTTTGTCTG-----	1068	
DB	823	CGGTGTGCTGTGTCGCCCGAGACACCGGCTGGGCGGGGTGGAAGAGGCGACTTCCGAGCA	882	
QY	1069	CATCTCTTCTCTCTAATAATGACTGGAACAACAATTGTATCTCTCTCCCCCTTTCGTT	1128	
DB	883	CATCTCTTCTCTTGTGGCTGTGACTGTGAATGTCTCCGGAGACAGCGTGGCCCCCTTTTACA	942	

QY 1129 CCCACCTCAAGTCTGACGATGACACTTCCATTGGA 1166
DB 943 CCGGATTTGGAAGGTGCGCACCGACATGCACTTGA 980

RESULT 13
US-08-422-706B-8
; Sequence 8, Application US/08422706B
; Patent No. 5977333
; GENERAL INFORMATION:
; APPLICANT: Brook, J. David
; APPLICANT: Housman, David E.
; APPLICANT: Shaw, Duncan J.
; APPLICANT: Harley, Helen J.
; APPLICANT: Johnson, Kelch J.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
; TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02713

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995

CLASSIFICATION: 435
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992

ATTORNEY/AGENT INFORMATION:
NAME: Grenahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1746
US-08-422-706B-8

Query Match 3.5%; Score 214; DB 2; Length 2511;

Best Local Similarity 54.2%; Pred. No. 8.6e-49;
Matches 508; Conservative 0; Mismatches 415; Indels 15; Gaps 3;

QY 244 GACACCATAGTCTGAGTATGAGAGCTCCAGCTTGGCAAAGACTTCCAGATCAGAAGT 303
DB 43 GCCATGCTGTAGAGCTTAAAGAGGTCCGACTGACAGAGGAGACTTCCAGATTCGAAG 102

QY 304 CTGTAGTGTGTGTGTCTTGTCTGTAAGTGCAGGTGTGAAGAGAAACCAACCGGGGAC 363
DB 103 GTGATGAGAGCGGGCGCTTCAAGAGGTAGCGGTATGTAAGATGAAGACAGAGGCGAC 162

QY 364 ATCTATGCTATGAAAAGTGAAGAAGAGGCTTTATTGCGCCAGAGGAGGTTTCATTT 423
DB 163 GTGTATGCTATGAAAGTATGAAAGTGGGACATCTTAAGAGGCGGAGGTGTGTG 222

QY 424 TTGAGAAAGAGCGGAATATTATCTGAAAGACAGAGCCGTGTGATCCCAATTACAG 483
DB 223 TTCGTGAGAGAGGAGCGTGTGTGAATGGGAGCGGCGGTGTATCAGCAGCTGCAC 282

QY 484 TATGCTTTCAGAGACAAATGACCTTTATCTGATGAGAGAAATGACGCTGAGGGGAC 543
DB 283 TTGCGCTTCAGAGATGAGAACTACCTGTACTGTGTATGATGATTAAGTGGCGGAGAC 342

QY 544 TTGCTGTCACTTTTGAATGATATGAGACCAAGTTAGTAAACCTGTATACATTTTAC 603
DB 343 CTGCTACACTGCTGAGCAAGTTGGGAGCGGATTCGGCGGAGATGGCGGCTTCTAC 402

QY 604 CTAGTGAAGTATTTTGTGCTGTTCACAGCGTTATCTGATGAGATAGCTGATCGAGAC 663
DB 403 CTGGCGGAGATTTGTCAATGAGCACTGCTGACCGGCTTGTGCTACGTCACAGGGAC 462

QY 664 ATCAAGCTGAGAAACATCTGCTGTCGCGGACAGACACATCAAGCTGTGTGATTTGGA 723
DB 463 ATCAAGCTGAGAAACATCTGCTGTCGCGGACAGACATCTGCTGTGCTGCTGCTGCTG 522

QY 724 TCTGCGCGGAAATGAAATCAAAAGATGATGATGCAAACTCCGATTTGGAGCCCA 783
DB 523 TCTGCTCTCAAGTGTGGGCGAGATGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582

QY 784 GATTACATGAGCTCTGCA---AGTGTGACTGTGATGAAAGCGGAGTGAAGACCTTAC 840
DB 583 GACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642

QY 841 GAGCTGAGCTGATCTGT 900
DB 643 GGGCCCGAGTGTGATGT 702

QY 901 TCCCGCTTGCAGAGGGAACCTGTGCAGAACTTCAATTAATTAATTAATTAATTAATTA 960
DB 703 AGCGCTTTCAGCGGAGATTCAGAGCGGAGACCTATGGAAGATCTCCACTCAAGAG 762

QY 961 TTTTGAATTCAGATGACCCCAAGTGAAGAGT---GACTTTTGTATGATTCATCA 1017
DB 763 CACCTCTCTGTGCGCTGTGTGAGCAAGGGGTCTCTGAGAGAGCTGAGACTTCATTCAG 822

QY 1018 AGCTTGT 1068
DB 823 CGGTTGT 882

QY 1069 CATCTTTCTTCTCTAAATATGAGTGAACCAATTCGTAATCTCTCTCTCTCTCTCTCT 1128
DB 883 CATCTTTCTTCTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 942

QY 1129 CCCACCTCAAGTCTGACGATGACACTTCCATTGGA 1166
DB 943 CCGGATTTGGAAGGTGCGCACCGACATGCACTTGA 980

RESULT 14
US-08-484-044-11
; Sequence 11, Application US/08484044
; Patent No. 5552282
; GENERAL INFORMATION:

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; APPLICANT: Caskey, C. T.
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Friedman, David L.
; APPLICANT: Pizzuti, Antonio
; APPLICANT: Fennick, Raymond G.
; TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
; NUMBER OF SEQUENCE: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,044
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/019,940
; FILING DATE: 19-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5443
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-484-044-11

Query Match      3.5%; Score 213.6; DB 1; Length 3182;
Best Local Similarity 54.2%; Pred. No. 1.3e-48;
Matches 507; Conservative 0; Mismatches 414; Indels 15; Gaps 3;

QY 246 CACCATAGCTAGTACAGAGAGCTCCAGCTTCGGCAAGAGCTTCGAAGTCAAGTCT 305
DB 743 CATCTGTGAGAGCTTAAGAGAGCTCCGACTGACAGAGGACGACTTCGAGATTCTGAAGT 802
QY 306 TGTAGGTTGTGTCACCTTGTGTAAGTGCAGGTGGTAAAGAGAGCAACCGGGAGCAT 365
DB 803 GATCGAGCGCGGGGCTTACAGAGAGTAGCGTAGTGAAGATGAAGACAGCGGCAAGT 862
QY 366 CATCTGTAGAAAGTGAAGAGAGAGGCTTTATTGGCCGAGAGAGGTTTCAATTTT 425
DB 863 GATTCCTATGAAGATCATGAACAGTGGACATCTGAAGAGGCGAGGTGTGCTT 922
QY 426 TGAGGAAGAGCGGAACATATTATCTCGAAGCAAGCCCGTGTGATCCCAATTACAGTA 485
DB 923 CGGTAGAGAGAGAGAGCTGTGTGTGAATGGGAGCCGGGGTGAATCAAGCAAGCTGCACCT 982
QY 486 TGCCTTTAGAGCAAAAAATCACTTTATCTGATGAGAGAAATACGCTGAGAGGAGACTT 545
DB 983 CGCCTTCCAGAGTGAAGACTACCTGTACCTGTATGAGATTAACGTGGGCGGGAGACT 1042
QY 546 GCTGTCACTTTTGAATAGATATAGAGACCAAGTTAGATAAAACTGATACAGTTTACTT 605
DB 1043 GCTGACACTGTGAGCAAGTTGGGAGCGGATTCGGGCGAGATGGCGCGCTTCACT 1102
QY 606 AGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATGTGAGGATACGTCATCGAGCAT 665

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DB 1103 GCGGAGATTGTCATAGCCCATAGACTCGGTGACCGGCTTGGCTACGTGCACAGGAGCAT 1162
QY 666 CAAGCTGAGAACATTTCTGTTGACCGGACAGAGACATCAAGCTGTGATTTTGGATC 725
DB 1163 CAACCCGACAAATCTCTGCTGACCGCTGTGGCCACATCCGCTGCGGCACTTTCGCTC 1222
QY 726 TGCCTGAAATGAATTTCAACAGATGTGAATCCAAACTCCGATTGGAGCCCAAGA 785
DB 1223 TTGCTTCAAGCTGCGGAGAGATGGAACGGTGTGCTGTGTGTGTGGGACCCCAAGA 1282
QY 786 TTACATAGGCTCTGA---AGTGTGACTGTATGAACGGGAGATGGAAGGCACTAGG 842
DB 1283 CTACCTGTCTCCCGAGATCTCTGACAGCTGTGTGGCCGTGGCTGAGACAGGAGCTACGG 1342
QY 843 CCTGGACTGTGACTGTGTGTGATGAGTGGCGGTGATTTGCTTATGATATTTTATGAGATC 902
DB 1343 GCCGAGTGTGACTGTGTGTGGGCTGTGGTGTATTTGCTTATGAATTTTATGAGCAAC 1402
QY 903 CCCCTTGCAGAGGAGAACTCTGCCAACACTTCAATATCAATTTATGAAATTTTCAGCGGTT 962
DB 1403 GCCCTTCAAGCGGATTTCCAGCGGAGAGACTATGGCAAGATGTCACATCAAGAGACA 1462
QY 963 TTTGAATTTTCCAGATGACCCCAAGTGAAGAGT---GACTTGTGATCTGATTTCAAG 1019
DB 1463 CCTCTCTGTGCTGCTGTGTGAGACAGAGGCTCTGAGAGAGCTGAGACTTCATTACAGG 1522
QY 1020 CTGTTGTGCGGCGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGEC-----CA 1070
DB 1523 GTTGCTGTGCTCCCGGAGACACAGGCTGGGCGGGGTGAGACAGGCGACTTCGGAGACA 1582
QY 1071 TCCCTTCTCTCTAAATTTGACTGGAACACATTCGTACTCTCTCCCTTCGTTCC 1130
DB 1583 TCCCTTCTCTTTGGCCCTGACTGAGATGTCTCCGGAGACGCTGCCCCCTTTACACC 1642
QY 1131 CACCCTCAAGTCTGACATGACACCTTCAATTTTGA 1166
DB 1643 GGATTTGGAAGTGCACCCGACATGCAATTTGA 1678

RESULT 15
US-09-804-471A-3
; Sequence 3, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) .. (174493)
; OTHER INFORMATION: n = A, T, C or G
US-09-804-471A-3

Query Match      3.3%; Score 205; DB 4; Length 174493;
Best Local Similarity 100.0%; Pred. No. 6.5e-45;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 753 GGTGAATGCCAAACTCCGATTTGGAGCCCGAGATTAATGAGCTCCGGAAGTGTGACTGT 812
DB 130289 GGTGAATGCCAAACTCCGATTTGGAGCCCGAGATTAATGAGCTCCGGAAGTGTGACTGT 130348
QY 813 GATGAACGGGAGATGAAAAAGACCTTAGCGCTGACTGTGATGTGTGTGAGTGGGCGT 872

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Db 130349 GATGAACGGGGATGGAAGCACTACGGCTGACTGTGACTGGTCAAGTGGCGT 130408
 Qy 873 GATTGGCTATGAGATGATTTATGGGATCCCCCTTGGCAGAGGGAACCTTGGCCAGAAC 932
 Db 130409 GATTGGCTATGAGATGATTTATGGGATCCCCCTTGGCAGAGGGAACCTTGGCCAGAAC 130468
 Qy 933 CTTCAATACATTATGAAATTTCCAG 957
 Db 130469 CTTCAATACATTATGAAATTTCCAG 130493

Search completed: March 2, 2005, 17:05:19
 Job time : 902.401 secs

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